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(54) **ADENO-ASSOCIATED VIRUS VIRIONS WITH VARIANT CAPSID AND METHODS OF USE THEREOF**

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None  
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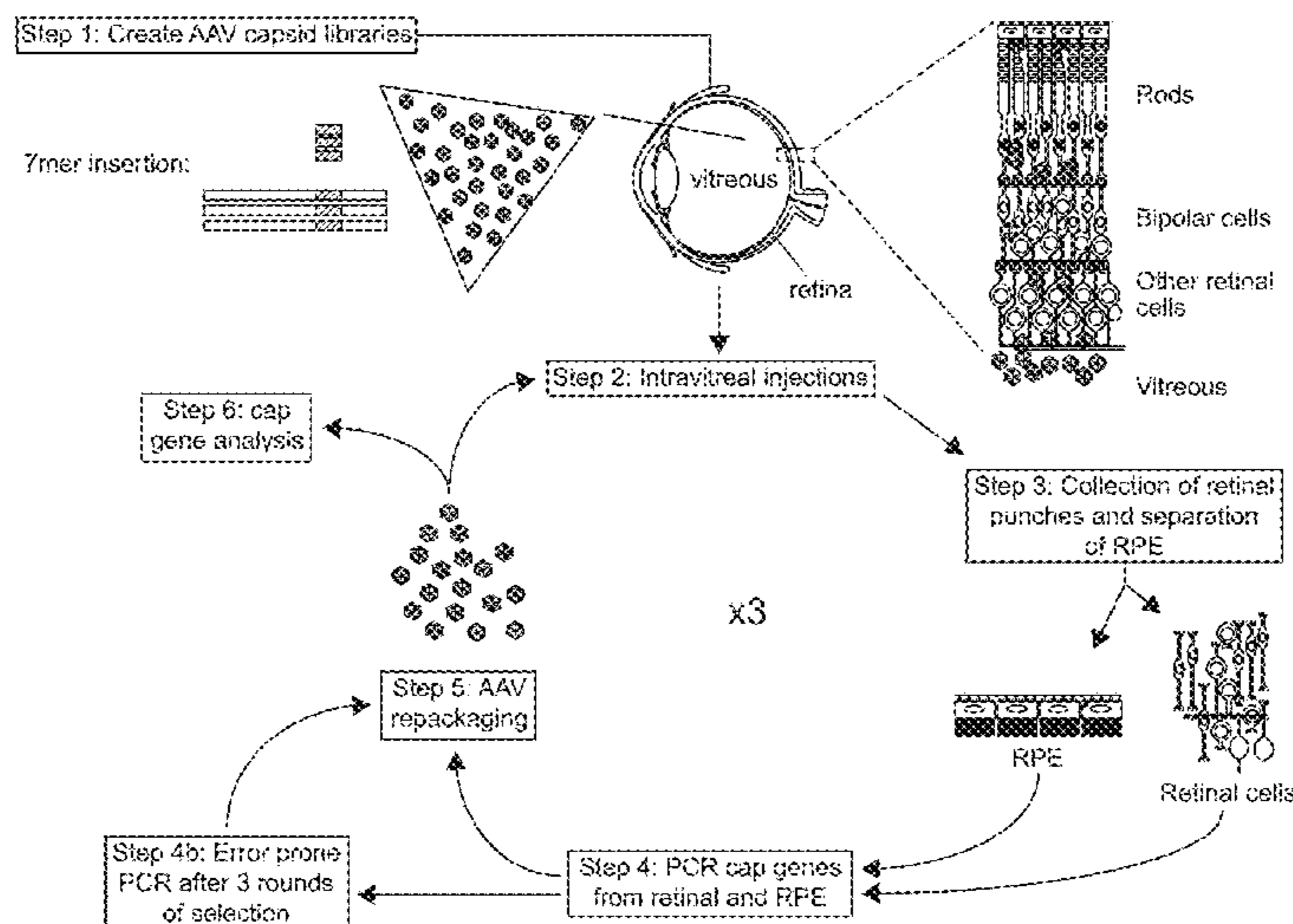
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(57) **ABSTRACT**

The present disclosure provides adeno-associated virus (AAV) virions with altered capsid protein, where the AAV virions exhibit greater infectivity of retinal cells compared to wild-type AAV. The present disclosure further provides methods of delivering a gene product to a retinal cell in an individual, and methods of treating ocular disease.

**15 Claims, 27 Drawing Sheets**

**Specification includes a Sequence Listing.**



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\* cited by examiner

FIG. 1

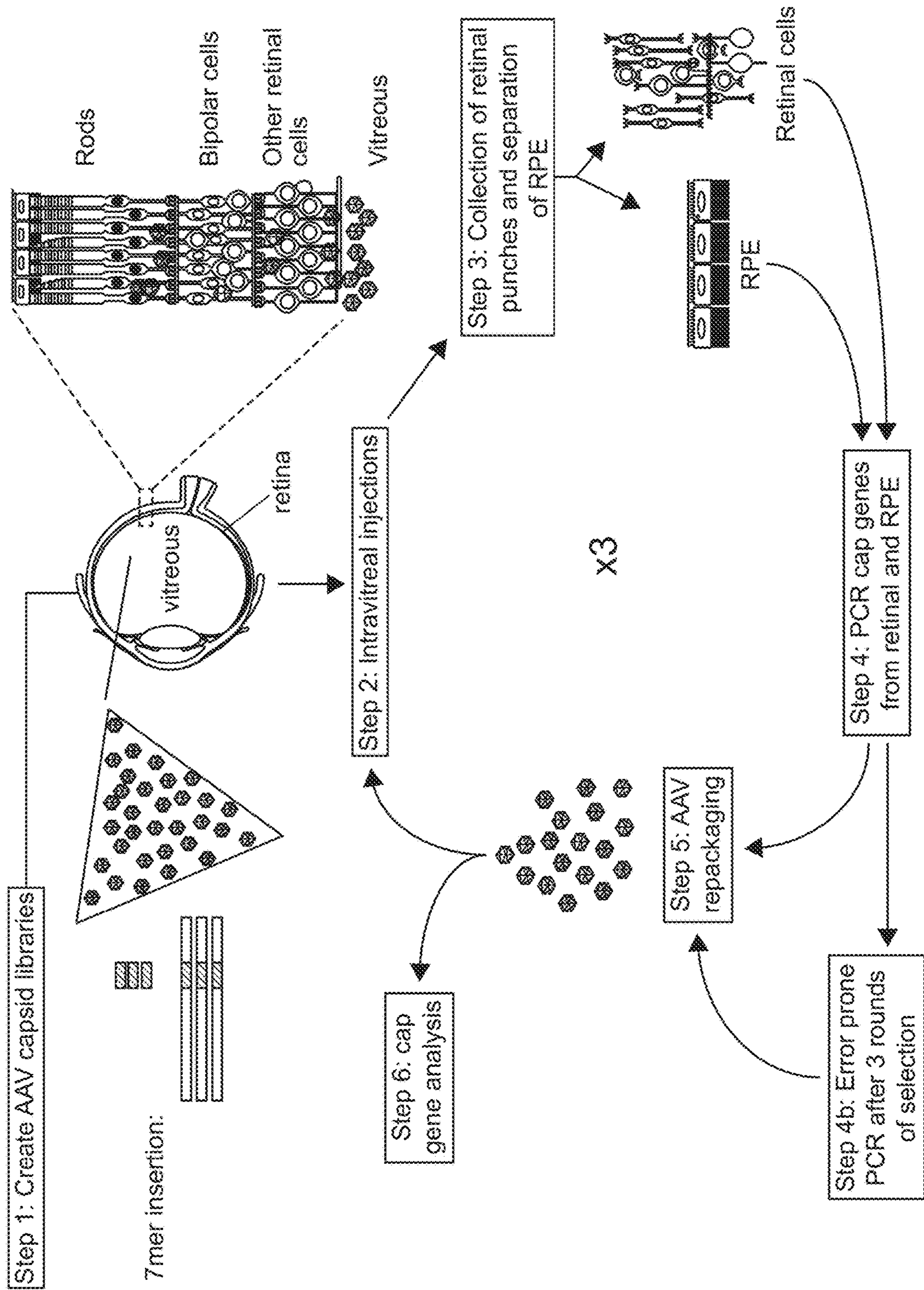


FIG. 2

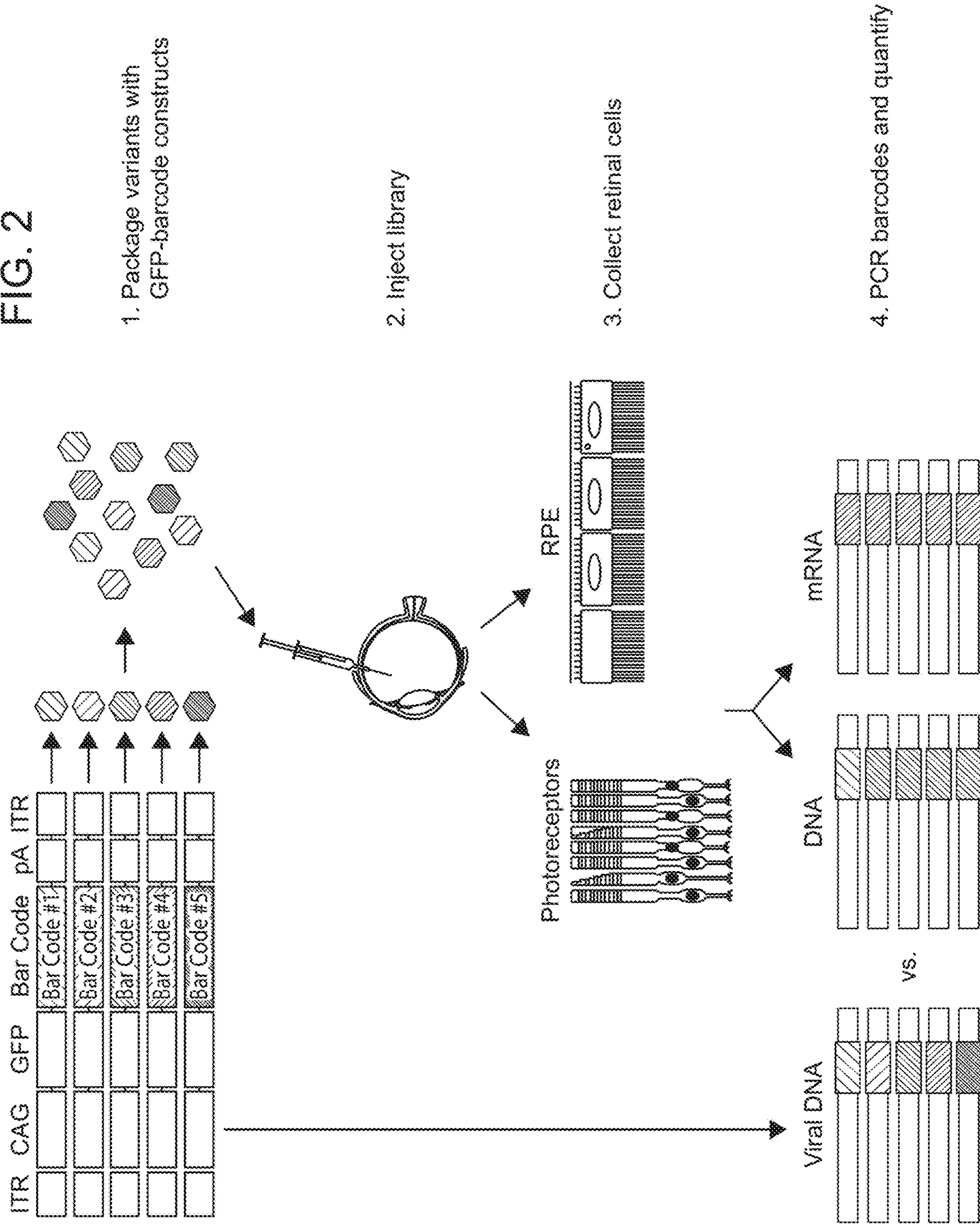
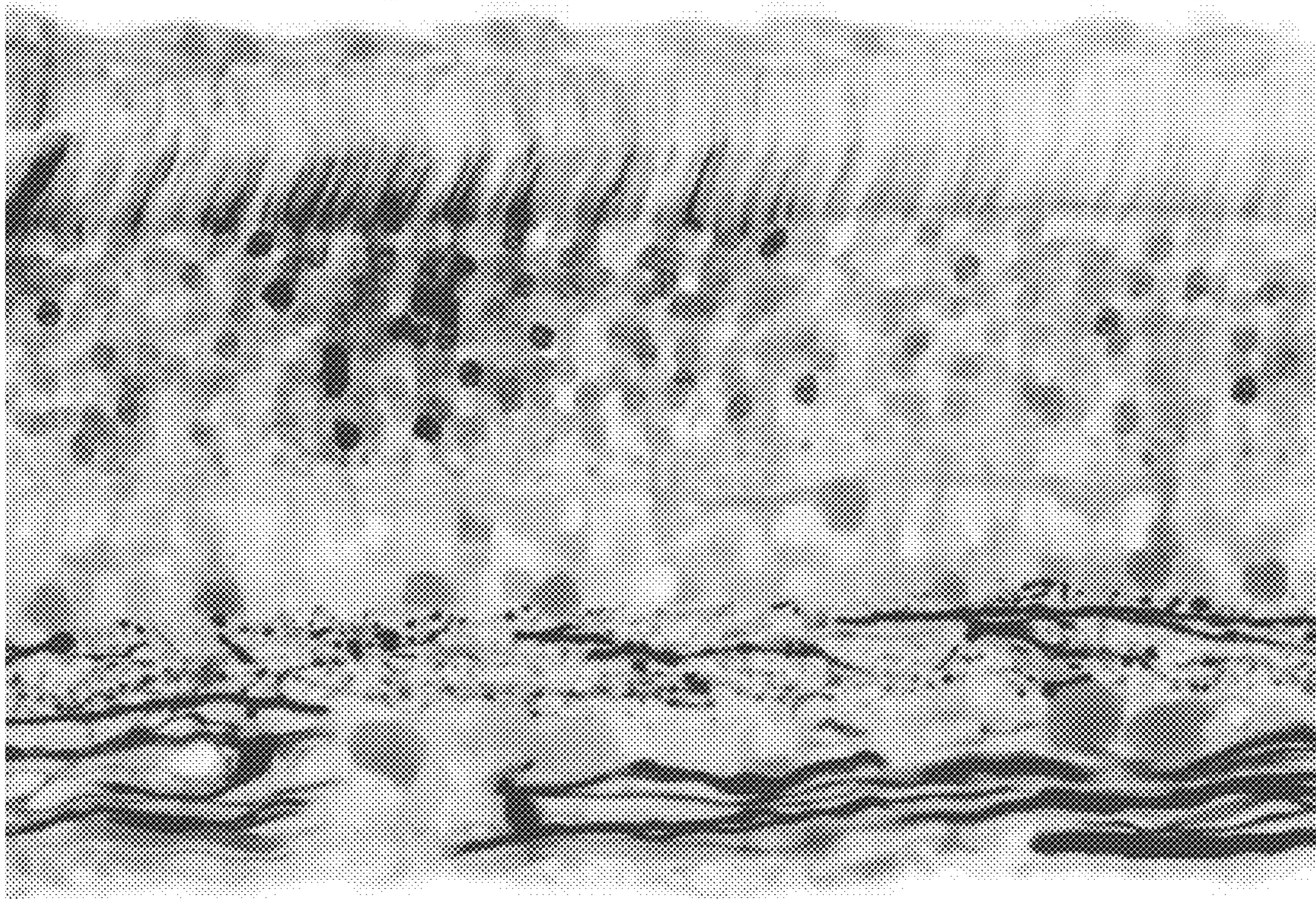




FIG. 3



20  $\mu\text{m}$

FIG. 4

AAV2 VP1 1 MAADGYLPDWLEDTLSEGIRQWVKLKPGPPPKPAERHKDDSRGLVLPGYKYLGFENGLD  
AAV2 VP1 61 KGEVNEADAAALEHDKAYDRQLDSGDNPLYLKYNHADAFAERLKEDETSFGGNLGRAVFQ  
AAV2 VP1 121 AKKRVLEPLGLVEEVPKTA PGKKRVEHSEVPEPSSSGTGKAGQQPARKRLNFGQTGDAD  
AAV2 VP1 181 SVPDEQPLGQPPAAPSGLTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI  
AAV2 VP1 241 TTSTRTWALPTYNNHLYKQISSQSGASNDNHYFGYSTPWGYDFNRFHCHFSPRDWQRLLI  
AAV2 VP1 301 NNNWGFRRPKRLNEKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG  
AAV2 VP1 361 CLPFFPADVFMVPQYGYLLTNNNGSQAVGRSSFYCLEYFPSQMLRTGNNTFSYTFEDVPF  
AAV2 VP1 421 HSSYAHSQSLDRLMNPLIDQYLYLSRTNTPSGTTQSRQLQFSQAGASDIRDQSRNWLPG  
AAV2 VP1 481 PCYRQQRVSKTSADNNNSEYSWTGATKYHLNGRDSLVPNGPAMASHKDDDEEKFPPQSGVL  
AAV2 VP1 541 IFGKQGSEKTNVDIEKVMITDEEEI RTTNPFVATEQYGSVSTNLQRGNRQAATADVNTQGV  
AAV2 VP1 601 LPGMVWQDRDVYLLQGP IWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTFVPANPSTT  
AAV2 VP1 661 FSAAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKS VNVDFTVDTNGVY  
AAV2 VP1 721 SEPRPIGTRYLFR (SEQ ID NO:1)

FIG. 5

AAV-2 570 PVATEQYGSVSTNLQRNRQAATADVNTQGVLPGMVWQDRDV 611 (SEQ ID NO:2)

AAV-1 571 PVATERFGTVAVNFQSSSTDPATGDVHAMGALPGMVWQDRDV 612 (SEQ ID NO:3)

AAV-5 560 RVAYNVGGQMATNNQSSTAPATGTYNLQEIIVPGSVWMERDV 601 (SEQ ID NO:4)

AAV-6 571 PVATERFGTVAVNLOSSSTDPATGDVHVMGALPGMVWQDRDV 612 (SEQ ID NO:5)

AAV-7 572 PVATEEYGIVSSNLQAANTAAQTQVVNNQGALPGMVWQNRDV 613 (SEQ ID NO:6)

AAV-8 573 PVATEEYGIVADNLQQNTAPQIGTVNSQGALPGMVWQNRDV 614 (SEQ ID NO:7)

AAV-9 571 PVATESYQQVATNHQSAQAQAQTGWVQNGILPGMVWQDRDV 612 (SEQ ID NO:8)

AAV-10 573 PVATEQYGVVADNLQQANTGPIVGNVNSQGALPGMVWQNRDV 614 (SEQ ID NO:9)

FIG. 6A

AAV1 --TFSYTFEEVPFHSSYAHSSQSLDRMLMNPLIDQYLYLNRTO-NQSSAQNKDLLFSRGS 467  
AAV6 --TFSYTFEEDVPFHSSYAHSSQSLDRMLMNPLIDQYLYLNRTO-NQSSAQNKDLLFSRGS 467  
AAV3 --TFSYTFEEDVPFHSSYAHSSQSLDRMLMNPLIDQYLYLNRTOGTTSGTTNQSRLLFSQAG 467  
AAV2 --TFSYTFEEDVPFHSSYAHSSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTQSRLLQFSQAG 466  
AAV8 NQFTYTFEEDVPFHSSYAHSSQSLDRMLMNPLIDQYLYLSRTQT-GGTANTQTLGFSQGG 469  
AAV8 .1 NQFTYTFEEDVPFHSSYAHSSQSLDRMLMNPLIDQYLYLSRTQT-GGTANTQTLGFSQGG 469  
AAV8 rh8 FQFSYTFEEDVPFHSSYAHSSQSLDRMLMNPLIDQYLYLVRTQTGTGGTQLAFSQAGPS 469  
AAV10 NEFFSYTFEEDVPFHSSYAHSSQSLDRMLMNPLIDQYLYLSRTQST-GGTQGTQLAFSQAG 469  
AAV7 -FEFSYSFEEDVPFHSSYAHSSQSLDRMLMNPLIDQYLYLARTQSNPCTAGNRELQFYQGG 469  
AAV9 -FQFSYEFENVPFHSSYAHSSQSLDRMLMNPLIDQYLYLSKTI--NGSGQNQTLKFSVAG 467  
AAV9 .1 -FQFSYEFENVPFHSSYAHSSQSLDRMLMNPLIDQYLYLSKTI--NGSGQNQTLKFSVAG 467  
AAV5 NEFFTYNFEEDVPFHSSYAHSSQSLDRMLMNPLIDQYLYRFSVTN-----NTGGVQFNKNL 453  
\*:\*

AAV1 PAGMSVQPKNWLPGCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESINPGTAMASH 527  
AAV6 PAGMSVQPKNWLPGCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESINPGTAMASH 527  
AAV3 PQMSLQARNWLPGCYRQQRVSKTANDNNNSNFPWTAAASKYHLNGRDLSLVNPGPAMASH 527  
AAV2 ASDIRDQSRNWLPGCYRQQRVSKTSADNNNSSEYSWGATKYHLNGRDLSLVNPGPAMASH 526  
AAV8 PNTMANQAKNWLPGCYRQQRVSTTTGQNNNSNEFAWTAGTKYHLNGRNSLANPGIAMATH 529  
AAV8 .1 PNTMANQAKNWLPGCYRQQRVSTTTGQNNNSNEFAWTAGTKYHLNGRNSLANPGIAMATH 529  
AAV8 rh8 S--MANQARNWVPPGCYRQQRVSTTTNQNNSNFAWTGAAKFKLNGRDSLMPGVAMASH 527  
AAV10 PANMSAQAKNWLPGCYRQQRVSTTLLSQNNNSNFAWTGATKYHLNGRDLSLVNPGVAMATH 529  
AAV7 PSTMAEQAKNWLPGCFRQQRVSKTLDQNNNSNFAWTGATKYHLNGRNSLVNPGVAMATH 529  
AAV9 PSNMAVQGRNYIPGPSYRQQRVSTTVTQNNNSSEFAWPFGASSWALNGRNSLMNPGPAMASH 527  
AAV9 .1 PSNMAVQGRNYIPGPSYRQQRVSTTVTQNNNSSEFAWPFGASSWALNGRNSLMNPGPAMASH 527  
AAV5 AGRYANTYKNWFPGPMGRTOGWNLGSGVNRAVSFAFATTNRMELEGASYQVPPQPNGMTN 513  
. :\*: \*:\*:\*:\*:\*:\*:\*:\*:\*:\*. \* . . . . . . . . . \* :\*:\*:



FIG. 6C

AAV1	PQILLIK-	650	(SEQ	ID	NO: 35)
AAV6	PQILLIK-	650	(SEQ	ID	NO: 36)
AAV3	PQIMIK-	650	(SEQ	ID	NO: 37)
AAV2	PQILLIKN	650	(SEQ	ID	NO: 38)
AAV8	PQILLIKN	653	(SEQ	ID	NO: 39)
AAV8.1	PQILLIKN	653	(SEQ	ID	NO: 40)
AAV8 rh8	PQILLIKN	651	(SEQ	ID	NO: 41)
AAV10	PQILLIKN	653	(SEQ	ID	NO: 42)
AAV7	PQILLIKN	652	(SEQ	ID	NO: 43)
AAV9	PQILLIK-	650	(SEQ	ID	NO: 44)
AAV9.1	PQILLIK-	650	(SEQ	ID	NO: 45)
AAV5	PMMLIKN	640	(SEQ	ID	NO: 46)

\* : : \* \* \*

FIG. 7A

**Retinoschisin-1**

*Homo sapiens*

```

1  msrkiegfll  lllfgyeatl  glsstedege  dpwyqkackc  dcqggpnalw  sagatsldci
61  pecpyhkpig  fesgevtpdq  itcsnpeqyv  gwysswtank  arlnsqgfgc  awlskfqdss
121 qwlqidlkei  kvisgiltqg  rcdidewmtk  ysvqyrtder  lnwiyykdqt  gnnrvfygns
181 drtstvqnll  rppiisrfir  liplgwhvri  airmellecv  skca (SEQ ID NO:10)

```

FIG. 7B

**BDNF**

*Homo sapiens*

```

1  mtillfltmvi  syfgcmkaap  mkeanirgqg  glaypgvrth  gtlesvngpk  agsrgitsla
61  dtfehvieel  ldedhkvrpn  eennkdadly  tsrvmlssqv  pleppllfll  eeyknyldaa
121 nmsmvlrhs  dparrgelsv  cdsisewvta  adkktavdms  ggtvtvlekv  pvskgqikqy
181 fyetkcnpmg  ytkegcrgid  krhwnsqcrt  tqsyvraltm  dskkrigwrf  iridtsvct
241 Itikrgr (SEQ ID NO:11)

```

## FIG. 7C

RPE65

*Homo sapiens*

1 msiqvehpag gykklfetve elsspltahv tgriplwltg slircpggif evgsepfyhl  
 61 fdgqallhkf dfkeghvtyh rrfirtdayv ramtekriivi tefgtcafpd pcknifsrff  
 121 syfrgvevtd nalvnvypvg edyyactetn fitkinpetl etikqvdi cn yvsvngatah  
 181 phiendgtvy nigncfgknf siaynivkip plqadkedpi skseivvqfp csdrfkpsyv  
 241 hsfgltpnyi vfvetpvkin lfkflsswsl wganymdcfe snetmgvwlh iadkkrkkyl  
 301 nnkyrtspfn lfhhintyed ngflivdlcc wkgfefvyny lylanlrenw eevkknarka  
 361 pqpevrryvl plnidkadtg knlvtlpntt atailcsdet iwlepevifs gprqafefpq  
 421 inyqkycgkp ytyayglgln hfvpdrllckl nvtketwvw qepdsypsep ifvshpdale  
 481 eddgvvlsvv vspgagqkpa yllilnakdl sevaraeevi nipvtfhgif kks  
 (SEQ ID NO:12)

## FIG. 7D

Peripherin-2

*Homo sapiens*

1 mallikvkfdq kkrvklaggI wlmnwfsvla giifslglf lkielkrksd vmnnseshfv  
 61 pnsligmgvl scvfnsIagk icydalDpak yarwkpwlkp ylaicvlfni ilflvalccf  
 121 llrgslentl gggIknmgky yrdtdtpgrc fmkktidmlq iefkccgng frdwfeiqwi  
 181 snryldfssk evkdrIksnv dgryIvdgvp fscnpsspr pciqyqitnn sahysydhqt  
 241 eelnIwvrgc raallsyys lmnsmgvvtl liwIfevtit iglrylqtSl dgvsnppeese  
 301 sesqgwIler svpetwkafI esvkkIqkgn qveaegadag qapeag (SEQ ID NO:13)



FIG. 7E

Peripherin  
*Homo sapiens*

```

1  mshhpsqira gfsstsyrrt fgpppslspg afsysssrff sssrllqgas psssvrlgsf
61  rspragagal lrlpserldf smaeanqgef latrsnekqe lqelndrfan fiekvrflaq
121 qnaalrgels qargqepara dqlcqqelre lrrelellgr erdrvqverd glaedlaalk
181 qrleeetrkr edaehnlvlf rkdvddatls rlelerkies lmdeliefikk lheeelrdlq
241 vsvesqqvqq veveatvkpe ltaalrdira qyesiaaknl qeaeewyksk yadlsdaanr
301 nhealrqakq emnesrrqiq sltcevdgir gtneallrql releeqfale aggyqagaar
361 leeelrqike emarhireyq ellnvkmaid ieiatyrkll egeesrisvp vhsfaslnik
421 ttvpeveppq dshsrktvli ktietrngev vtesqkeqrs eldkssahsy (SEQ ID NO:14)

```

## FIG. 7F

**RPGR-interacting protein-1**  
*Homo sapiens*

1 mshlvdptsg dlpvrdidai plvlpaskgk nmktqpplsr mnreeledsf frlredhmlv  
 61 kelswkqqde ikrlrttllr ltaagrdirv aeeaaplset arrgqkagwr qrlsmhqrpq  
 121 mhrlqghfhc vgpasprraq prvqvghrql htagapvpek pkrqprdris ytappsfkeh  
 181 atnenrgeva skpselvsqs nsisfssvi smakpiglcm pnsahimasn tmqveeppks  
 241 pekmpkden feqrsleca qkaaelrasi kekvelirrk kllhernasl vmtkaqltev  
 301 qeayetllqk nqgilsaah allkqvnelr aelkeeskka vslksqledv silqmtlikef  
 361 qervedleke rkllndnydk llesmldssd sssqphwsne liaeqlqqqv sqlqddqdae  
 421 ledkrkvllle lsrekaqned lklevtnilq khkqevellq naatisqppd rqsepathpa  
 481 vlqentqiep sepknqeekk lsqvlnelqv shaettlele ktrdmlilqr kinvcyqeel  
 541 eamntkadnd nrdhkekler ltrlldlkn rikqlegilr shdipstseql kdwaygtrpi  
 601 slcletlpah gdedkvdisi lhqgenlfel hihqafitsa alaqagdtqp ttftctysfyd  
 661 fethctplsv gpqplydfts qyvmetdsif ihylqeasar ldihqamase hstlaagwic  
 721 fdrvletvek vhglatliga ggeefgvley wmlrfpikp slqacnkrkk agvylstdvl  
 781 ggrkaqeeef rseswepqne lwieitkccg lrsrwlgtqp spyavyrfft fsdhdtaaip  
 841 asnnpyfrdq arfpvlvtst ldhylrreal sihvfdedi epgsylgrar vpllplakne  
 901 sikgdfnlt dpaekpngsiq vqldwkfpyi ppefllkpea qtkgkdtkds skisseeka  
 961 sfpsqdqmas pevpleaggy rskrkpphgg erkekehqv sysrrkhgkr igvqgknrme  
 1021 ylslnlimgn tpeqvnyte w kfsetnsfig dgfknqheee emtlshsalk qkeplhpvnd  
 1081 kesseggev seaqtdsdd vivppmsqky pkadseknci eivslafype aevmsdenik  
 1141 qyveykfyd lplsetetpv slrkpragee ihfhfskvid ldpqeqqgrr rflfdmlngq  
 1201 dpdqghlkft vvsdpldeek keceevgyay lqlwqilesq rdileqeidi vspedlatpi  
 1261 grlkvslqaa avlhaiykem tedifs (SEQ ID NO:15)

## FIG. 7G

**Rab escort protein-1**

1 madtlpsefd vivigtglpe siaaacrs grrvlhvdsr sygggnwasf sfsgllswlk  
61 eyqensdivs dspvwqdqil eneeaialsr kdktiqhvev fcyasqdlhe dveeagalqk  
121 nhalvtsans teaadsaflp tedeslstms cemlteqtps sdpenalevn gaevtgeken  
181 hddkktcvps tsaedmsenv piaedtteqp kknritysqi ikegrfrnid lvskllysrq  
241 llidlliksn vsryaefkni trilafrgr veqvpcsrad vfnskqltmv ekrmimkflt  
301 fcmeyekypd eykgyeeitf ye1lktqklt pnlqyivmhs iamtsetass tidglikatkn  
361 flhclgrygn tpflflygq gelpqcfcrm cavfggiycl rhsvqclvvd kesrkckail  
421 dqfggriise hflvedsyfp enmcsrvqyr qisravlitd rsvlktddsq qisiltpae  
481 epgtfavrvi elcsstmtcm kgtylvhltc tssktaredl esvvqklfvp ytemeieneq  
541 vekprilwal yfnmrdssdi srscyndlps nvvcsppdc glgndnavkq aetlfqeicp  
601 nedfcppppn pediildgds lqpeassa ipeansetfk estnignlee sse

(SEQ ID NO:16)

**FIG. 7H****212-amino acid isoform of RdCVF**

1 maslfsgril irnnsdqdel dteaevsrri enrlvllffg agacpqcqaf vpilkdffvr  
61 ltdefyvlra aqlalvyvsq dsteeqqdlf lkdkmpkkwlf lpfeddlrrd lgrqfsverl  
121 pavvvlkpdg dvltrdgade iqrlgtacfa nwqeaavld rnfqlpedle dgeprsltec  
181 lrrhkyrvek aarggrdp9g gggeeggagg lf (SEQ ID NO:17)

**FIG. 7I****156-amino acid isoform of RdCVF (isoform 1)**

1 mvdilgerhl vtckgatvea eaalqnkva lyfaaarcap srdftpllcd fytalvaea  
61 rpapfevvfv sadgssqeml dfmrelhgaw lalpfdhpyr helrkrynvt aipklvkvq  
121 ngevitnkr qqirerqlac fqdwveaadi fqnfsv (SEQ ID NO:18)

**FIG. 7J****135-amino acid isoform of RdCVF (isoform 2)**

1 mvdilgerhl vtckgatvea eaalqnkva lyfaaarcap srdftpllcd fytalvaea  
61 rpapfevvfv sadgssqeml dfmrelhgaw lalpfdhpyr qrsllalprl ecsgvilahc  
121 nlcilgssds lalas (SEQ ID NO:19)

## FIG. 7K

Rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha (PDE6 $\alpha$ )  
 GenBank NP\_00431

```

1  mgevtaeeve kfldsnigfa kyyynlhya klisdllgak eaavdfsnyh spssmeesei
61  ifdllrdfqe nlqtekcihn vmkklcflly adrmslfmyr trngiaelat rlfnvhkday
121 ledclvmpdq eivfpdmgi vghvahskki anvpnteede hfcdfvdiilt eytknilas
181 pimngkdvva iimavnkvdg shftkrdeei ilkylnfanl imkvyhlsyl hncetrrgqi
241 llwsgskvfe eltdierqfh kalytvrafl ncdrysvgll dmtkqkeffd vwpvlmgevvp
301 pysgprtpdg reinfykvid yilhgkedik vipnpppdhw alvsglpayv aqnglicnim
361 napaedffaf qkepldesgw miknvlsmpl vnkkeivgv atfynrkdgk pfdemdetlm
421 esltqflgws vlnpdtyesm nklenrkdif qdivkyhvk c dneeiqkilk trevygkepwp
481 eceeeelaei lqaelpdadk yeinkfhfsd lpltelelvk c giqmyyelk vvdckfhlpqe
541 alvrfmysls kgyrkityhn wrhgfsvgqt mfsllvtgki kryftdleal amvtaafchd
601 idhrgtnnly qmksqnplak lhgssilerh hlefgktllr desinifqnl nrrqhehaih
661 mmdiaiatd lalyfkkrtm fqkivdqskt yeseqewtqy mmleqtrkei vmammntacd
721 lsaitkpwev qsqvallvaa efweqgdler tvlqqnppm mdrnkadelp klqvgfidfv
781 ctfvykefsr fheetpml d gitnrrkewk aladeydakm kvqeekkkqkq qsaksaaagn
841 qpggnpspgg attskscclq (SEQ ID NO:20)

```

## FIG. 7L

Rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit beta isoform 1 (PDE6 $\beta$  isoform 1)  
 GenBank NP\_000274

```

1  mslseeqars fldqnpdfar qyfgkkispe nvaacedgc ppdcdsirdl cqveestall
61  elvqdmqesi nmervvfkvl rriictliqad rcslfmyrqr ngvaeiatrl fsvqpdsvle
121  dclvppdsei vfldigvvg hvaqtkkmvn vedvaecephf ssfadeltdy ktknmlatpi
181  mngkdvvavi mavnklnqpf ftsededvfl kynfatllyl kiyhlsylhn cetrergvll
241  wsankvfeel tdierqfhka fytvraylnc erysvglldm tkekeffdvw svlmgessqpy
301  sgprtpdgre ivfykvidyi lhgkeekivi ptpsadhwal asglpsyvae sgficnimna
361  sademfkfge galdsgwli knvlsmpi.vn kkeei.vgvat fynrkdgkpf degdevlmes
421  ltqflgwsvm ntdtydkmnk lenrkdiagd mvlyhvkcdr deiqlilptr arlgkepadc
481  dedelgeilk eelpgpttfd iyefhfsdle cteldlvkcg iqmyyielgvv rkfgipqevl
541  vrfifsiskg yrrityhnwr hgfnvaqtmf tilmtgkks yytdleafam vtaglchdid
601  hrgtnnlyqm ksqnplaklh gssilerhhl efgkflisee tlniyqnlnr rqhehvihlm
661  diaiatdia lyfkkramfq kivedsknyq dkkswveyls lettrkeivm ammntacdls
721  aitkpwevqs kvallvaaef weggdlertv ldqqpipmnd rnkaaelpk1 qvgfidfvct
781  fvykefsrfh eeilpmfdr1 qnnrkewkal adeyeakvka leekeeeerv aakkvgteic
841  nggpapksst ccil (SEQ ID NO:21)

```

## FIG. 7M

Rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit beta isoform 2 (PDE6 $\beta$  isoform 2)  
 GenBank NP\_001138763

```

1  mslseeqars fldqnpdfar qyfgkklspe nvaacedgc ppdcslrdl cqveestall
61  elvqdmqesi nmervvfkvl rrlctllqad rcslfmyrqr ngvaelatrl fsvqpdsvle
121 dclvppdsei vfpldigvvg hvaqtkkmvn vedvaecephf ssfadeltdy ktknmlatpi
181 mngkdvvavi mavnklnqpf ftsededvfl kylnfatlyl kiyhlsylhn cetrngqvll
241 wsankvfeel tdierqfhka fytvraylnc erysvglldm tkekeffdvw svlmgescpy
301 sgprtpdgre ivfykvidyi lhgkeekvi ptpsadhwal asglpsyvae sgfincimna
361 sademfkfqe galddsgwli knvlsmpivn kkeeivgvat fynrkdgkpf deqdevlmes
421 ltqflgwsvm ntddydkmnk lenrkdiagd mvlvkvkcdm deiqllilptr arlgkepadc
481 dedelgeilk eelppgttfd iyefhfsdie cteldlvkcg iqmyyelgvv rkfqipqevl
541 vrfifsiskg yrrityhnwr hgfnvaqtmf tllmtgkiks yytdleafam vtaglchdid
601 hrgttnlyqm ksqnplaklh gssilerhhl efgkflisee tlniyqnlnr rqhehvihlm
661 diaiiaatdla lyfkkrampf kivdesknyq dkkswveyls lettrkeivm ammtacdls
721 aitkpwvqqs kvallvaaef weqgdlertv ldqqpipmmd rnkaaelplk qvgfidfvct
781 fvykefsrfh eeilpmfdr1 qnnrkewkal adeyeakvka ieekeeeerv aakkgteicn
841 ggpapksstc cil (SEQ ID NO:22)

```

## FIG. 7N

Rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit beta isoform 3 (PDE6 $\beta$  isoform 3)  
GenBank NP\_001138764

```

1  mtkekefdv  wsvlmgessqp  ysgprtpdgr  eivfykvidy  ilhgkeekv  iptpsadhwa
61  lasglpsyva  esgficnimm  asademfkfq  egaldsdgwl  iknvlsm piv  nkkeei v gva
121  tfynrkdgkp  fdeqdevlme  sitqflgsv  mntdtydkm  klenrkdi aq  dmvlyhvkcd
181  rdeiqllipt  rarlgkepad  cdedelgeil  keelpgpttf  diyefhfsd l  ecteldlvkc
241  giqmyyelgv  vrkqipqev  lvrflfsisk  gyrrityhnw  rhgnvvaqtm  ftllmtgk lk
301  syytdleafa  mvtaglchdi  dhrgttnlyq  mksqnlakl  hgssilerhh  lefgkfllse
361  etlniyqnl  rrqhehvihl  mdiailatdl  alyfkkramf  qkivdeskny  qdkkswvey l
421  slettrkeiv  mammtacdl  saitkpwevq  skvallvaae  fweqgdle r t  vldqqpipmm
481  drnkaaelpk  lqvffidfvc  tfvykefsrf  heeillpmfdr  lqnrkewka  ladeyeakvk
541  aleekeeer  vaakkvgtei  cnggpapkss  tccil (SEQ ID NO:23)

```

## FIG. 7O

Cyclic nucleotide-gated cation channel alpha-3 isoform 1 (CNGA3 isoform 1)  
GenBank NP\_001289

```

1  makintqysh  psrthlkvkt  sdrdlnraen  glsrahssse  etssvlqpgi  ametrgiads
61  qqsftqggi  arlsrlfll  rrwaarhvhh  qdggpdsfpd  rfrgaelkev  ssqesnaqan
121  vgsqepadrg  rsawplakcn  tntsnnteee  ktkkkkdaiv  vdpssnlyyr  wltaialp vf
181  ynwyllicra  cfdehqseyl  mlwlvldysa  dvlyvldvlv  rartgfl e qg  lmvstdtnrlw
241  qhyktttqfk  ldvlslvptd  laylkvgtny  pevrfnrlk  fsrlfeffdr  tetrtnypnm
301  frignlvlyi  liihwnaci  yfaiskfigf  gtdswvypni  sipehgrlsr  kyislywst
361  ltlttigetp  ppvkdeeylf  vvvdflvgvl  ifativgnvg  smisnmnasr  aefgakidsi
421  kqymqfrkvt  kdletrvirw  fdylwankkt  vdekevlksl  pdklkaeiai  nvhldtlk kv
481  rifqdceagl  lvelvlklrp  tvfspgdyic  kkgdigkemy  iinegklavv  addgvtqfvv
541  lsdgsyfgei  silnikgks  gnrrtanirs  igysdlfcls  kddlmealte  ypeakkalee
601  kgrqilmkdn  liddeelarag  adpkdleekv  eqlgssldtl  qtrfarllae  ynatqmkmkq
661  rlsqlesqvk  ggdgkpladg  evpgdatkte  dkqq (SEQ ID NO:24)

```



## FIG. 7P

Cyclic nucleotide-gated cation channel alpha-3 isoform 2 (CNGA3 isoform 2)  
GenBank NP\_001073347

```
1  makintqysh psrthlkvkt sdrdlnraen glsrahssse etssvliqpgi ametrglads
61  gqgsftgqgi arlsrlifll rrwaarhvh qdqgpdspfd rfrgaelkev ssqesnaqan
121 vgsqepadrg rrkttkkkda ivvdpsnly yrwltaialp vfynwyllic racfdelqse
181 ylmwlvidy sadvlyvidv lvrartgflv lkfsrlfeff drtetrttq nmfrignlvi yiliihwna
241 tdlaylkvgt nypevrrfnrl nisipehgrl srkyiyslyw stltlttge tpppvkdeey
301 ciyfaiskfi gfgtdswvyp vlifativgn vgsminma sraefqakid sikqymqfrk vtkdletarvi
361 lfvvvdflvg ktvdekevlk slpdllkaei ainvhldtlk kvrifqdcea glivelvkl
421 rptvfpdgy ickkgdigke myiinegkla vvaddgvtqf vvlsgdgsyfg eisiiniqgs
541 ksgnrrtani rsiqysdlfc lskddlmeal teypeakkai eekgrqilmk dnliideelar
601 agadpkdlee kveqlgssld tlqtrfarll aeynatqmkm kqrlsqlesq vkgggdkpla
661 dgevpgdatk tedkqq (SEQ ID NO:25)
```

## FIG. 7Q

Cyclic nucleotide-gated cation channel beta-3 (CNGB3)  
GenBank NP\_061971

```

1  mfksttkvnk vkpigenen eqssrneeg shpsnsgqt taqeenkee kslktkstpv
61  tseephtniq dklskknsg dltnpdpqn aaeptgtvpe qkempgkeg pnsqknkppa
121  apvineyada qlhnlvkrmr qrtalykkl. vegdlsspea spqtakptav ppvkesddkp
181  tehyyrllwf kvkkmpltey lkrklpnsi dsytdrlyll wlllvtlayn wnccfiprlr
241  vfpvyqtadni hyladiic diilyldmlf iqprlqfvrq gdiivdsnel rkhyrtstkf
301  qldvasiipf dicylffgfn pmfranrmk ytsffefnhh iesimdkayi yrvirttgyi
361  lfilhinacv yywasnyegi gtrwvydge gneylrcyyw avrtlitigg lpepqtlfel
421  vfqlinffsg vfvfssliqq mrdvigaata nqnyfracmd dtiaymnnys ipklvqkrvr
481  twyeytwdsq rmidesllk tlpttvqlal aidvnfsiis kvdlfkgcdt qmiydmllrl
541  ksvlylpgdf vckkgeigke myiikhgevq vlggpdgtkv lvtlkagsvf geisllaagg
601  gnrrtanvva hgfanlltld kktlqeilvh ypdserilmk karvllkqka ktaeatpprk
661  dlallfppke etpklfktll ggtgkaslar llkikregaa qkkensegge eegkenedkq
721  kenedkqken edkgkenedk dkgrepeekp ldrpectasp iaveeeephsv rrtvlprgts
781  rqsliismap saeggeevlt ievkekakq (SEQ ID NO:26)

```

## FIG. 7R

Guanine nucleotide-binding protein G(t) subunit alpha-2 (GNAT2)  
GenBank NP\_005263

```

1  mgsgasaedk elakrskele kklqedadke aktvkl11lg agesgstiv kqmkiihqdg
61  yspeeclefk aiylgnvlqs ilairamtt lgidyapesc addgrqinnl adsieegtmp
121  pelvevirrl wkdgqvqacf eraaeyqlnd sasyylnqle ritdpeylps eqdvirsrvk
181  ttgiietkfs vkdlnfrmfv vggqrserkk whncfegvte iifcaalsay dmlveddev
241  nrmheslhif nsicnhkffa atsilflnk kdlfeekikk vhlscfpey dggnsyddag
301  nyiksqfldl nmrkdvkeiy shmtcatdtq nvkfvfdavt diikenlkd cglf
      (SEQ ID NO:27)

```

## FIG. 7S

RPGR -- 815 amino acids  
 GenBank NP\_000319

1 mrepeelmpd sgavftfgks kfaennpgkf wfkndvpvhl scgdehsavv tgnnklymfq  
 61 snnwggqlglg sksaiskptc vkalkpekvk laacgrnhtl vsteggnavya tggnnegqlg  
 121 lgdteerntf hvistftseh kikqlsagsn tsaaltdgr lfmwgdnsseg qiglnknsnv  
 181 cvpqqvtigk pvswiscgyy hsafvttdge lyvfgepeng klglpnqllg nhrtplqvse  
 241 ipekviqvac ggehtvvlte navytfglgq fgqlglgtfl fetsepkvie nirdqtisiy  
 301 scgenhtali tdiglmtyfg dgrhgklglg lenfnhhfip tlcsnflrfi vklvacggch  
 361 mvvfaaphrg vakeiefdei ndtclsvatf lpyssltsgn vlqrtlrsarm rrrererspd  
 421 sfsmrrtlpp iegtlglisac flpnsvfprc sernlqesvl seqdlmqpee pdyllidemtk  
 481 eaaidnsstv eslgettdil nmthinslns neksklspv qkqkkqgtig eltqdtalte  
 541 nddsdeyeem semkegkack qhvsqgifmt qpattieafs deeveipeek egaedskng  
 601 ieeqeveane envkvhggrk ekteiilsddl tdkaedhefs kteelkledv deenaenve  
 661 skkktvgdde svptgyhskt egaertndds saetiekkk anleeraice ynenpkgyml  
 721 ddadssslei iensettpsk dmkktkkifl fkrvpsinqk ivknnneplp eiksiggdqi  
 781 lksdnkdadq nhmsqnhqni pptnterrsk sctil (SEQ ID NO:28)

## FIG. 7T

RPGR – 646 amino acids  
GenBank CAB54002

```

1 mrepeelmpd sgavftfgks kfaennpgkf wfkndvpvhl scgdehsavv tgnnklymfg
61 snnwggqlgig sksaiskptc vkalkpekvk laacgrnhtl vsteggnvya tggnnegqlg
121 lgdteerntf hviisftseh kikqlsagen tsaaltdedgr lfmwgdnsseg qiglknvsnv
181 cvpqqvtigk pvswiscgyy hsafvttdge lyvfgepeng klglpnqllg nhrtplvse
241 ipekviqvac ggehvtvltte navytfglgq fgqlglgtfl fetsepkvie nirdqtisiy
301 scgenhtali tdiglmytfg dgrhgklglg lenfthhfip tlcsnflrfi vklvacggch
361 mvvfaaphrg vakeiefdei ndtclsvatf lpyssltsgn vlqrtlsarm rrrerersp
421 sfsmrrtlpp iegtlglisac flpnsvfprc sernlqesvl seqdlmqpee pdyllidemtk
481 eaeidnsstv eslgettdil nmthimslns nekslklsqv qkqkkqqtig eltqdtalte
541 nddsdeyeem semkegkack qhvsqgifmt qpattieafs deeveipeek egaedskgng
601 ieeqeveane envkvhggrr ekteiisddl tdkaeysash sqivsv (SEQ ID NO:29)

```

FIG. 7U

RPGR – 1152 amino acids

1 mrepeelmpd sgavftfgks kfaennpgkf wfkndvpvhl scgdehsavv tgnnklymfg  
 61 snnwqqlglg sksaiskptc vkalkpekvk laacgrnhtl vsteggnavya tggnnegqlg  
 121 lgdteerntf hvisfftseh kikqlisagsn tsaaltedgr lfmwgdnsseg qiglknvsnv  
 181 cvpqqvtigk pvswiscggy hsafvttdge iyvfgepeng klglpnqllg nhrtpqlvse  
 241 ipekviqvac ggehtvvlte navytfglgq fgqlglgtfl fetsepkvie nirdqtisyi  
 301 scgenhtali tdiglmtytfg dgrhgklglg lenfnhfip tlcsnflrfi vklvacggch  
 361 mvvfaaphrg vakeiefdei ndtclsvatf lpyssltsgn vlqrtltsarm rrrererspd  
 421 sfsmrrtlpp iegtlglisac flpnsvfprc sernlqesvl seqdlmqpee pdylldemtk  
 481 eaaidnsstv eslgettdil nmthimslns nekslklspv qkqkkqqtig eltqdtalte  
 541 nddsdeyeem semkegkack qhvsqgifmt qpattieafs deeveipeek egaedskgng  
 601 ieegeveane envkvhggrk ekteiilsddi tdkaevsegk aksvgeaedg pegrgdgtce  
 661 egssgaeahwq deerekgek krgemerpg egekelaeke ewkkrdgeeq eqkeregghq  
 721 kernqemeeg geeehgegee eegdreeeee kegegkeege geevegerek eegekkeer  
 781 agkeekgeee gdqgegeeee tegrgeekke egeveggeve egkgereeee eegegeeeeeg  
 841 egeeegege eegegkgee egegegeeee egegegeee eegegeeee gegegeeeeeg  
 901 egegeeegeg egeeegegk geegegegeg egeeegege gedgegegee eegevegeeee  
 961 egegegeee egegegege geegegegeg eeegegeege eegegeeee gegeeeeeeeg  
 1021 vegevegeeg egevegeeee egevegeeee eegeeeegkyq etgeeeenerq  
 1081 dgeeykkvsk ikgsvkygkh ktyqkksvtn tqngkqrs kmpvqskrll kngpsgskkf  
 1141 wnnvlphyle ik (SEQ ID NO:30)

## FIG. 7V

## RPGR – 1020 amino acids

1 mrepeeimpd sgavftfgks kfaennpgkf wfkndvpvhl scgdehsavv tgnnklymfg  
 61 snnwggqiglg sksaiskptc vkalkpekvk laacgrnhtl vsteggnavya tggnnegqig  
 121 lgdteerntf hvisfftseh kikqlsagsn tsaaltedgr ifmwgdnsseg qigiknvsnv  
 181 cvpqqvtigk pvswiscgyy hsafvttdge lyvfgepeng klglpnqllg nhrtpqlvse  
 241 ipekviqvac ggehtvvlte navytfglgq fgqlglgtfl fetsepkvie nirdqtiysi  
 301 scgenhtali tdiglmtytfg dgrhgklglg ienfnhfip tlcsnflrfi vklvacggch  
 361 mvvfaaphrg vakeiefdei ndtclsvatf lpyssitsgn vlqrtlisarm rrrererspd  
 421 sfsmrrtlpp iegtlglisac flpnsvfprc sernlqesvi seqdlmqpee pdylidemtk  
 481 eaeidnsstv eslgettdil nmthimslns nekslklsqv kqkkkqgtig eltqdtalte  
 541 nddsdeyeem semkegkack qhvsqgfmt qpattieafs deevgndtgq vgpqadtgde  
 601 glqkevyrhe nngvdqlda keiekesdgg hsqkeseaee idseketkla eiagmkdlre  
 661 rekstkkmsp ffgnlpdrgm nteseenkdf vkkresckqd vifdseresv ekpdsymega  
 721 sesqqgiadg fqqpeaiefs sgekedeve tdqniirygrk lieqqneket kpiisksmak  
 781 ydfkcdrlse ipeekegaed skngieeeg veaneenvkv hggrkektei lsddltdkae  
 841 dhefskteel kledvdeein aenveskkt vgddevptg yhsktegaer tnddssaeti  
 901 ekkekanlee raiceytenp kgymlddads ssleilense ttpskdmkkt kkiflkrvp  
 961 sinqkivknn neplpeiiksi gdqiilkson kdadqnhmsq nhqniptnt errskstii

(SEQ ID NO:31)

## FIG. 8A

*Streptococcus pyogenes* Cas9

1 mdkkysigld igtntsvgwav itdeykvpsk kfkvlgntr hsikkniiga llfsggetae  
61 atrlkrtrr rytrrknric ylqeifsnem akvddsffhr leesflveed kkherhpfgr  
121 nivdevayhe kyptiyhrk klvdstdkad irliylalah mikfrghfli egdlpndnsd  
181 vdklfiqlvq tynqlfeenp inasgvdaka ilsarlsksr rlenliaqlp geknglfgn  
241 lialslgltp nfksnfdiae daklqlskdt ydddldnlla qigdgyadlf laaknlsdai  
301 llsdilirvnt eitkapsas mikrydehhq diltllkalvr qqlpekykei ffdqskngya  
361 gyidggasqe efykfikpil ekmdgteell vknredlir kqrtfdngsi phqihlgelh  
421 ailrrqedfy pflkdnreki ekiltfripv yvgplargns rfawmtrkse etitpwnfee  
481 vvdkgasaqs fiermtrfdk nlpnekvlpk hsllyeyftv yneltkvkvv tegmrkpafi  
541 sgeqkkaivd llfktnrkvt vkqlkedyfk kiecfdsvet sgvedrfnas lgtyhdlkik  
601 ikdkdfldne enedilediv ltltfedre mieerlktya hlfdkvmkq lkrtrytgwg  
661 rlsrklngi rdkqsgktil dflksdgfan rnfmglihd sltfkediqk aqvsgqgdsi  
721 nehianlags paikkgiliqt vkvvdelvkv mgrhkpeniv iemarenqtt qkgqknsrer  
781 mkrieegike lgsqilkehp ventqlqnek lylylqngr dmyvdqeldi nrlsdydvdh  
841 ivpqsflkdd sidnkvltrs dknrgksdntv pseevvkkmk nywrqlinak litqrkfdni  
901 tkaergglse ldkagfikrq lvetrqitkh vaqildsrnn tkydendkli revkvitlks  
961 klvsdfrkdf qfykvreinn yhhahdayln avvgtalikk ypklesefvy gdykvydvkr  
1021 miakseqeig katakyffys nimnffktei tiangeirkr plietngetg eivwdkgrdf  
1081 atvrkvlsmv qvnivkktev qtggfskesi ipkrnsdkli arkkdwdpkk yggfdsptva  
1141 ysvlvvakve kgskkkksv kelligitime rssfeknpid fleakgykev kkdliiklpk  
1201 yslfelengr krmlasagel qkgnelalps kyvnflylas hyeklkgspe dneqqlfve  
1261 qhkhyldeli eqisefskrv iladanldkv isaynkhrdk pireqaenii hlftltniga  
1321 paafkyfdtt idrkrytstk evldatlihg sitglyetri dlsqiggd (SEQ ID NO:32)

## FIG. 8B

*Staphylococcus aureus* Cas9

1 mkrnyllgld igitvgygi idyetrdiv agvrlfkean venngrsk rgarrikrrr  
61 rhriqrvkl lfdynltdh selsginpye arvkglsqkl seeefaall hlakrrgvhn  
121 vnevedtgn elstkeqisr nskaleekyv aelqlerlkk dgevrgsinr fktedyvkea  
181 kqllkvqkay hqidqsfidt yidlletrt yyegpgegsp fgwkdikewy emlmghctyf  
241 peelrsvkya ynadlynaln dlndlvtird enekleyyek fqienvfkk kkkptlkqia  
301 keillvneedi kgyrvtstgk peftnlkvyh dikditarke iienaelldq iakiltiyqs  
361 sediqaeltl nselteqei eqisnlkgyt gthnlsikai nllidelwht ndnqiaifnr  
421 lklvpkkvdl sqqkeipttl vddfllspvv krsfiqsikv inaiikkygl pndiieelar  
481 eknskdaqm inemqkrnrq tnerieeir ttgkenakyl iekiklhdmq egkclyslea  
541 ipledllnp fnyevdhiip rsvfdnsfn nkvlvqeen skgnrtfpq ylssdsksis  
601 yetfkkhiln lakggrisk tkkeylleer dinrfsvqkd finrnlvdtr yatrqlmlli  
661 rsyfrvnnld vkvksinggf tsflrrkwkf kkernkgykh haedalilian adfifkewkk  
721 ldkakkvmen qmfeekqaes mpeietegey keifitphqi khikdfkyk yshrvdkkpn  
781 relindtlys trkddkqntl ivnnlnglyd kdndkiklli nkspekllmy hhdppqyqki  
841 klimeqygde knplykyee tgnlytkysk kdngpvikki kyygnklinah lditddypns  
901 rnkvvklsik pyrfdvylnd gvykfvtkn ldvikkenyy evnskoyeea kllkksnqa  
961 efiasfynnd likingelyr vigvndlln rievnmidit yreylenmd krppriikti  
1021 asktqsikky stdilgnlye vkskhpqi kkg (SEQ ID NO:33)



## FIG. 8C

*Francisella tularensis* Cpfl

1 mslyqefvnk yslsktlrfe lipqktlen ikargliidd ekrakdykka kqiiddkyhqf  
 61 fieeillssvc isedllqnys dvyfklkksd ddnlqkdfks akdtikkqis eyikdsekfk  
 121 nlfqnllida kkggesdliil wlqskdngi elfkansdit didealeiik sfkgwttyfk  
 181 gfhenrknvy ssndiptsii yrivddnlpk flenkakyes ikdkapeain yeqikkdlae  
 241 eltfdidykt sevnqrvfsl devfeianfn nylngsgitk fntliiggkfv ngentkrkgi  
 301 neyinlysqq indktlkkyk msvlfkqils dtesksfvid kieddsdvvt tmqsfyeqia  
 361 afktveeksi ketlslldd lkaqldisk iyfkndkslt disqqvddy svigtavley  
 421 itqqiapknl dnpskkeqel iaktekaky lsletiklal eefnkhrdid kqcrfeeilla  
 481 nfaaipmifd eiaqkdnla qisikyqngg kkdllqasae ddvkaikdli dqtnnllhki  
 541 kifhisqsed kanildkdeh fylvfeecyf elanivplyn kirnyitqkp ysdekfklmf  
 601 enstlangwd knkepntai lfikdkyyl gvmnknnki fddkaikenk gegykkivyk  
 661 llpgankmlp kvffsaksik fynpsedilr irnhsthtkn gspqkyekf efniedcrkf  
 721 idfykqsisk hpewkdfgr fsdtqrynsi defyrevenq gykltfenis esyidsvvnq  
 781 gklylfqiyn kdfsayskgr pnhtlywka lfdernlqdv vyklngeael fyrkqsipkk  
 841 ithpakeaia nknkdpkke svfeydlikd krftedkfff hcptinfks sgankfndei  
 901 nllikekand vhlisidrge rhlayytlvd gkgniikqdt fniigndrmk tnyhdklaai  
 961 ekdrdsarkd wkkinnikem kegylsqvvh eiaklvieyn aivvfedlnf gfkrgfrkve  
 1021 kvyyqklekm lieklnylvf kdnefdktgg virayqltap fetfkkmgkq tgiyyvvpag  
 1081 ftskicpvtg fvnqlypkye svksqeffs kfdkicynid kgyfefsfdy knfgdkaakg  
 1141 kwttiasfgr linfrnsdkn hnwdtrevyp tkelekllkd ysieyghgec ikaaicgesd  
 1201 kkffakltsv lntilqmrrns ktgteldyli spvadvnfnf fdsrqapknm pqdadangay  
 1261 hlgikgimll griknqgegk klnlviknee yfefvqnrn (SEQ ID NO:34)

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**ADENO-ASSOCIATED VIRUS VIRIONS  
WITH VARIANT CAPSID AND METHODS OF  
USE THEREOF**

CROSS-REFERENCE

This application is continuation of U.S. application Ser. No. 16/315,032 filed Jan. 3, 2019, which application is a national stage filing under 35 U.S.C. § 371 of PCT/US2017/044206, filed Jul. 27, 2017, which claims the benefit of U.S. Provisional Patent Application No. 62/368,929, filed Jul. 29, 2016, which applications are incorporated herein by reference in their entirety.

STATEMENT REGARDING FEDERALLY  
SPONSORED RESEARCH

This invention was made with government support under Contract/Grant Nos. EY022975, EY018241 and EY006855 awarded by the National Institutes of Health. The government has certain rights in the invention.

INCORPORATION BY REFERENCE OF  
SEQUENCE LISTING PROVIDED AS A TEXT  
FILE

A Sequence Listing is provided herewith in a text file, BERK-335\_SEQ\_LISTING\_ST25, created on Jan. 3, 2019 and having a size of 208,613 bytes. The contents of the text file are incorporated herein by reference in its entirety.

INTRODUCTION

Photoreceptors are the first neurons in the retina to receive and process visual information, converting visible electromagnetic radiation into hyperpolarized responses through phototransduction. The overwhelming majority of inherited retinal diseases result in the loss of these cells, either directly, such as in dominant mutations that affect rhodopsin protein folding, or indirectly, such as in recessive mutations that affect retinal recycling pathways in the retinal pigment epithelium (RPE).

Adeno-associated virus (AAV) belongs to the Parvoviridae family and Dependovirus genus, whose members require co-infection with a helper virus such as adenovirus to promote replication, and AAV establishes a latent infection in the absence of a helper. Virions are composed of a 25 nm icosahedral capsid encompassing a 4.9 kb single-stranded DNA genome with two open reading frames: rep and cap. The non-structural rep gene encodes four regulatory proteins essential for viral replication, whereas cap encodes three structural proteins (VP1-3) that assemble into a 60-mer capsid shell. This viral capsid mediates the ability of AAV vectors to overcome many of the biological barriers of viral transduction-including cell surface receptor binding, endocytosis, intracellular trafficking, and unpackaging in the nucleus.

SUMMARY

The present disclosure provides recombinant adeno-associated virus (AAV) virions with altered capsid protein, where the recombinant AAV (rAAV) virions exhibit greater infectivity of a retinal cell compared to wild-type AAV, and where the rAAV virions comprise a heterologous nucleic acid. The present disclosure further provides methods of delivering a gene product to a retinal cell in an individual,

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and methods of treating ocular disease. The present disclosure provides an rAAV virion, where the rAAV virion exhibits at least 5-fold increased localization to one or more of the inner nuclear layer, the outer nuclear layer, the photoreceptor layer, the ganglion cell layer, and the retinal pigment epithelium, compared to the extent of localization to the inner nuclear layer, the outer nuclear layer, the photoreceptor layer, the ganglion cell layer, or the retinal pigment epithelium, by an AAV virion comprising the corresponding parental AAV capsid protein.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a schematic depiction of a directed evolution method used to develop AAV variants that exhibit increased infectivity of an ocular cell (e.g., a retinal cell), compared to the parental AAV.

FIG. 2 is a schematic depiction of deep sequencing of AAV variants containing green fluorescent protein (GFP)-barcode constructs.

FIG. 3 depicts infection of cells in the ganglion cell layer, the inner nuclear layer, the photoreceptor layer, and the retinal pigment epithelium (RPE) layer, by an 18-member AAV variant library.

FIG. 4 provides an amino acid sequence of AAV2 capsid protein VP1. Amino acids 587 and 588 (NP) are in bold and underlined.

FIG. 5 provides amino acid sequences corresponding to amino acids 570-610 of AAV capsid protein VP1 of various AAV serotypes.

FIG. 6A-6C provide an alignment of amino acid sequences of AAV capsid protein loop IV (GH loop) regions. Insertion sites are shown in bold and underlining. AAV1: SEQ ID NO:35; AAV6: SEQ ID NO:36; AAV3: SEQ ID NO:37; AAV2: SEQ ID NO:38; AAV8: SEQ ID NO:39; AAV8.1: SEQ ID NO:40; AAV8 rh8: SEQ ID NO:41; AAV10: SEQ ID NO:42; AAV7: SEQ ID NO:43; AAV9: SEQ ID NO:44; AAV 9.1: SEQ ID NO:45; AAV5: SEQ ID NO:46.

FIG. 7A-7V provide amino acid sequences of exemplary heterologous gene products.

FIG. 8A-8C provide amino acid sequences of exemplary guide-RNA-directed endonucleases.

DEFINITIONS

The term “retinal cell” can refer herein to any of the cell types that comprise the retina, such as retinal ganglion cells; amacrine cells; horizontal cells; bipolar cells; photoreceptor cells including rods and cones; Müller glial cells; astrocytes (e.g., a retinal astrocyte); and retinal pigment epithelium.

“AAV” is an abbreviation for adeno-associated virus, and may be used to refer to the virus itself or derivatives thereof. The term covers all subtypes and both naturally occurring and recombinant forms, except where required otherwise. The abbreviation “rAAV” refers to recombinant adeno-associated virus, also referred to as a recombinant AAV vector (or “rAAV vector”). The term “AAV” includes AAV type 1 (AAV-1), AAV type 2 (AAV-2), AAV type 3 (AAV-3), AAV type 4 (AAV-4), AAV type 5 (AAV-5), AAV type 6 (AAV-6), AAV type 7 (AAV-7), AAV type 8 (AAV-8), AAV type 9 (AAV-9), avian AAV, bovine AAV, canine AAV, equine AAV, primate AAV, non-primate AAV, and ovine AAV. “Primate AAV” refers to AAV isolated from a primate, “non-primate AAV” refers to AAV isolated from a non-primate mammal, “bovine AAV” refers to AAV isolated from a bovine mammal (e.g., a cow), etc.

An “rAAV vector” as used herein refers to an AAV vector comprising a polynucleotide sequence not of AAV origin (i.e., a polynucleotide heterologous to AAV), typically a sequence of interest for the genetic transformation of a cell. In general, the heterologous polynucleotide is flanked by at least one, and generally by two AAV inverted terminal repeat sequences (ITRs). The term rAAV vector encompasses both rAAV vector particles and rAAV vector plasmids.

An “AAV virus” or “AAV viral particle” or “rAAV vector particle” refers to a viral particle composed of at least one AAV capsid protein (typically by all of the capsid proteins of a wild-type AAV) and an encapsidated polynucleotide rAAV vector. If the particle comprises a heterologous polynucleotide (i.e. a polynucleotide other than a wild-type AAV genome, such as a transgene to be delivered to a mammalian cell), it is typically referred to as an “rAAV vector particle” or simply an “rAAV vector”. Thus, production of rAAV particle necessarily includes production of rAAV vector, as such a vector is contained within an rAAV particle.

“Packaging” refers to a series of intracellular events that result in the assembly and encapsidation of an AAV particle.

AAV “rep” and “cap” genes refer to polynucleotide sequences encoding replication and encapsidation proteins of adeno-associated virus. AAV rep and cap are referred to herein as AAV “packaging genes.”

A “helper virus” for AAV refers to a virus that allows AAV (e.g. wild-type AAV) to be replicated and packaged by a mammalian cell. A variety of such helper viruses for AAV are known in the art, including adenoviruses, herpesviruses and poxviruses such as vaccinia. The adenoviruses encompass a number of different subgroups, although Adenovirus type 5 of subgroup C is most commonly used. Numerous adenoviruses of human, non-human mammalian and avian origin are known and available from depositories such as the ATCC. Viruses of the herpes family include, for example, herpes simplex viruses (HSV) and Epstein-Barr viruses (EBV), as well as cytomegaloviruses (CMV) and pseudorabies viruses (PRV); which are also available from depositories such as ATCC.

“Helper virus function(s)” refers to function(s) encoded in a helper virus genome which allow AAV replication and packaging (in conjunction with other requirements for replication and packaging described herein). As described herein, “helper virus function” may be provided in a number of ways, including by providing helper virus or providing, for example, polynucleotide sequences encoding the requisite function(s) to a producer cell in trans.

An “infectious” virus or viral particle is one that comprises a polynucleotide component which it is capable of delivering into a cell for which the viral species is tropic. The term does not necessarily imply any replication capacity of the virus. As used herein, an “infectious” virus or viral particle is one that can access a target cell, can infect a target cell, and can express a heterologous nucleic acid in a target cell. Thus, “infectivity” refers to the ability of a viral particle to access a target cell, infect a target cell, and express a heterologous nucleic acid in a target cell. Infectivity can refer to in vitro infectivity or in vivo infectivity. Assays for counting infectious viral particles are described elsewhere in this disclosure and in the art. Viral infectivity can be expressed as the ratio of infectious viral particles to total viral particles. Total viral particles can be expressed as the number of viral genome (vg) copies. The ability of a viral particle to express a heterologous nucleic acid in a cell can be referred to as “transduction.” The ability of a viral particle to express a heterologous nucleic acid in a cell can be assayed using a number of techniques, including assessment

of a marker gene, such as a green fluorescent protein (GFP) assay (e.g., where the virus comprises a nucleotide sequence encoding GFP), where GFP is produced in a cell infected with the viral particle and is detected and/or measured; or the measurement of a produced protein, for example by an enzyme-linked immunosorbent assay (ELISA). Viral infectivity can be expressed as the ratio of infectious viral particles to total viral particles. Methods of determining the ratio of infectious viral particle to total viral particle are known in the art. See, e.g., Grainger et al. (2005) *Mol. Ther.* 11:S337 (describing a TCID50 infectious titer assay); and Zolotukhin et al. (1999) *Gene Ther.* 6:973.

A “replication-competent” virus (e.g. a replication-competent AAV) refers to a phenotypically wild-type virus that is infectious, and is also capable of being replicated in an infected cell (i.e. in the presence of a helper virus or helper virus functions). In the case of AAV, replication competence generally requires the presence of functional AAV packaging genes. In general, rAAV vectors as described herein are replication-incompetent in mammalian cells (especially in human cells) by virtue of the lack of one or more AAV packaging genes. Typically, such rAAV vectors lack any AAV packaging gene sequences in order to minimize the possibility that replication competent AAV are generated by recombination between AAV packaging genes and an incoming rAAV vector. In many embodiments, rAAV vector preparations as described herein are those which contain few if any replication competent AAV (rcAAV, also referred to as RCA) (e.g., less than about 1 rcAAV per  $10^2$  rAAV particles, less than about 1 rcAAV per  $10^4$  rAAV particles, less than about 1 rcAAV per  $10^8$  rAAV particles, less than about 1 rcAAV per  $10^{12}$  rAAV particles, or no rcAAV).

The term “polynucleotide” refers to a polymeric form of nucleotides of any length, including deoxyribonucleotides or ribonucleotides, or analogs thereof. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs, and may be interrupted by non-nucleotide components. If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. The term polynucleotide, as used herein, refers interchangeably to double- and single-stranded molecules. Unless otherwise specified or required, any embodiment of the invention described herein that is a polynucleotide encompasses both the double-stranded form and each of two complementary single-stranded forms known or predicted to make up the double-stranded form.

A polynucleotide or polypeptide has a certain percent “sequence identity” to another polynucleotide or polypeptide, meaning that, when aligned, that percentage of bases or amino acids are the same when comparing the two sequences. Sequence similarity can be determined in a number of different manners. To determine sequence identity, sequences can be aligned using the methods and computer programs, including BLAST, available over the world wide web at [ncbi.nlm.nih.gov/BLAST/](http://ncbi.nlm.nih.gov/BLAST/). Another alignment algorithm is FASTA, available in the Genetics Computing Group (GCG) package, from Madison, Wis., USA, a wholly owned subsidiary of Oxford Molecular Group, Inc. Other techniques for alignment are described in *Methods in Enzymology*, vol. 266: Computer Methods for Macromolecular Sequence Analysis (1996), ed. Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, Calif., USA. Of particular interest are alignment programs that permit gaps in the sequence. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See *Meth. Mol. Biol.* 70: 173-187 (1997). Also, the GAP

program using the Needleman and Wunsch alignment method can be utilized to align sequences. See *J. Mol. Biol.* 48: 443-453 (1970)

Of interest is the BestFit program using the local homology algorithm of Smith Waterman (*Advances in Applied Mathematics* 2: 482-489 (1981)) to determine sequence identity. The gap generation penalty will generally range from 1 to 5, usually 2 to 4 and in many embodiments will be 3. The gap extension penalty will generally range from about 0.01 to 0.20 and in many instances will be 0.10. The program has default parameters determined by the sequences inputted to be compared. Preferably, the sequence identity is determined using the default parameters determined by the program. This program is available also from Genetics Computing Group (GCG) package, from Madison, Wis., USA.

Another program of interest is the FastDB algorithm. FastDB is described in *Current Methods in Sequence Comparison and Analysis, Macromolecule Sequencing and Synthesis, Selected Methods and Applications*, pp. 127-149, 1988, Alan R. Liss, Inc. Percent sequence identity is calculated by FastDB based upon the following parameters:

Mismatch Penalty: 1.00;  
Gap Penalty: 1.00;  
Gap Size Penalty: 0.33; and  
Joining Penalty: 30.0.

A "gene" refers to a polynucleotide containing at least one open reading frame that is capable of encoding a particular protein after being transcribed and translated.

The term "guide RNA", as used herein, refers to an RNA that comprises: i) an "activator" nucleotide sequence that binds to a guide RNA-directed endonuclease (e.g., a class 2 CRISPR/Cas endonuclease such as a type II, type V, or type VI CRISPR/Cas endonuclease) and activates the RNA-directed endonuclease; and ii) a "targeter" nucleotide sequence that comprises a nucleotide sequence that hybridizes with a target nucleic acid. The "activator" nucleotide sequence and the "targeter" nucleotide sequence can be on separate RNA molecules (e.g., a "dual-guide RNA"); or can be on the same RNA molecule (a "single-guide RNA").

A "small interfering" or "short interfering RNA" or siRNA is a RNA duplex of nucleotides that is targeted to a gene interest (a "target gene"). An "RNA duplex" refers to the structure formed by the complementary pairing between two regions of a RNA molecule. siRNA is "targeted" to a gene in that the nucleotide sequence of the duplex portion of the siRNA is complementary to a nucleotide sequence of the targeted gene. In some embodiments, the length of the duplex of siRNAs is less than 30 nucleotides. In some embodiments, the duplex can be 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11 or 10 nucleotides in length. In some embodiments, the length of the duplex is 19-25 nucleotides in length. The RNA duplex portion of the siRNA can be part of a hairpin structure. In addition to the duplex portion, the hairpin structure may contain a loop portion positioned between the two sequences that form the duplex. The loop can vary in length. In some embodiments the loop is 5, 6, 7, 8, 9, 10, 11, 12 or 13 nucleotides in length. The hairpin structure can also contain 3' or 5' overhang portions. In some embodiments, the overhang is a 3' or a 5' overhang 0, 1, 2, 3, 4 or 5 nucleotides in length.

As used herein, the term "microRNA" refers to any type of interfering RNAs, including but not limited to, endogenous microRNAs and artificial microRNAs (e.g., synthetic miRNAs). Endogenous microRNAs are small RNAs naturally encoded in the genome which are capable of modulating the productive utilization of mRNA. An artificial microRNA can be any type of RNA sequence, other than

endogenous microRNA, which is capable of modulating the activity of an mRNA. A microRNA sequence can be an RNA molecule composed of any one or more of these sequences. MicroRNA (or "miRNA") sequences have been described in publications such as Lim, et al., 2003, *Genes & Development*, 17, 991-1008, Lim et al., 2003, *Science*, 299, 1540, Lee and Ambrose, 2001, *Science*, 294, 862, Lau et al., 2001, *Science* 294, 858-861, Lagos-Quintana et al., 2002, *Current Biology*, 12, 735-739, Lagos-Quintana et al., 2001, *Science*, 294, 853-857, and Lagos-Quintana et al., 2003, *RNA*, 9, 175-179. Examples of microRNAs include any RNA that is a fragment of a larger RNA or is a miRNA, siRNA, stRNA, sncRNA, tncRNA, snoRNA, smRNA, shRNA, snRNA, or other small non-coding RNA. See, e.g., US Patent Applications 20050272923, 20050266552, 20050142581, and 20050075492. A "microRNA precursor" (or "pre-miRNA") refers to a nucleic acid having a stem-loop structure with a microRNA sequence incorporated therein. A "mature microRNA" (or "mature miRNA") includes a microRNA that has been cleaved from a microRNA precursor (a "pre-miRNA"), or that has been synthesized (e.g., synthesized in a laboratory by cell-free synthesis), and has a length of from about 19 nucleotides to about 27 nucleotides, e.g., a mature microRNA can have a length of 19 nt, 20 nt, 21 nt, 22 nt, 23 nt, 24 nt, 25 nt, 26 nt, or 27 nt. A mature microRNA can bind to a target mRNA and inhibit translation of the target mRNA.

"Recombinant," as applied to a polynucleotide means that the polynucleotide is the product of various combinations of cloning, restriction or ligation steps, and other procedures that result in a construct that is distinct from a polynucleotide found in nature. A recombinant virus is a viral particle comprising a recombinant polynucleotide. The terms respectively include replicates of the original polynucleotide construct and progeny of the original virus construct.

A "control element" or "control sequence" is a nucleotide sequence involved in an interaction of molecules that contributes to the functional regulation of a polynucleotide, including replication, duplication, transcription, splicing, translation, or degradation of the polynucleotide. The regulation may affect the frequency, speed, or specificity of the process, and may be enhancing or inhibitory in nature. Control elements known in the art include, for example, transcriptional regulatory sequences such as promoters and enhancers. A promoter is a DNA region capable under certain conditions of binding RNA polymerase and initiating transcription of a coding region usually located downstream (in the 3' direction) from the promoter.

"Operatively linked" or "operably linked" refers to a juxtaposition of genetic elements, wherein the elements are in a relationship permitting them to operate in the expected manner. For instance, a promoter is operatively linked to a coding region if the promoter helps initiate transcription of the coding sequence. There may be intervening residues between the promoter and coding region so long as this functional relationship is maintained.

An "expression vector" is a vector comprising a region which encodes a polypeptide of interest, and is used for effecting the expression of the protein in an intended target cell. An expression vector also comprises control elements operatively linked to the encoding region to facilitate expression of the protein in the target. The combination of control elements and a gene or genes to which they are operably linked for expression is sometimes referred to as an "expression cassette," a large number of which are known and available in the art or can be readily constructed from components that are available in the art.

“Heterologous” means derived from a genotypically distinct entity from that of the rest of the entity to which it is being compared. For example, a polynucleotide introduced by genetic engineering techniques into a plasmid or vector derived from a different species is a heterologous polynucleotide. A promoter removed from its native coding sequence and operatively linked to a coding sequence with which it is not naturally found linked is a heterologous promoter. Thus, for example, an rAAV that includes a heterologous nucleic acid encoding a heterologous gene product is an rAAV that includes a nucleic acid not normally included in a naturally-occurring, wild-type AAV, and the encoded heterologous gene product is a gene product not normally encoded by a naturally-occurring, wild-type AAV. As another example, a variant AAV capsid protein that comprises a heterologous peptide inserted into the GH loop of the capsid protein is a variant AAV capsid protein that includes an insertion of a peptide not normally included in a naturally-occurring, wild-type AAV.

The terms “genetic alteration” and “genetic modification” (and grammatical variants thereof), are used interchangeably herein to refer to a process wherein a genetic element (e.g., a polynucleotide) is introduced into a cell other than by mitosis or meiosis. The element may be heterologous to the cell, or it may be an additional copy or improved version of an element already present in the cell. Genetic alteration may be effected, for example, by transfecting a cell with a recombinant plasmid or other polynucleotide through any process known in the art, such as electroporation, calcium phosphate precipitation, or contacting with a polynucleotide-liposome complex. Genetic alteration may also be effected, for example, by transduction or infection with a DNA or RNA virus or viral vector. Generally, the genetic element is introduced into a chromosome or mini-chromosome in the cell; but any alteration that changes the phenotype and/or genotype of the cell and its progeny is included in this term.

A cell is said to be “stably” altered, transduced, genetically modified, or transformed with a genetic sequence if the sequence is available to perform its function during extended culture of the cell in vitro. Generally, such a cell is “heritably” altered (genetically modified) in that a genetic alteration is introduced which is also inheritable by progeny of the altered cell.

The terms “polypeptide,” “peptide,” and “protein” are used interchangeably herein to refer to polymers of amino acids of any length. The terms also encompass an amino acid polymer that has been modified; for example, disulfide bond formation, glycosylation, lipidation, phosphorylation, or conjugation with a labeling component. Polypeptides such as anti-angiogenic polypeptides, neuroprotective polypeptides, and the like, when discussed in the context of delivering a gene product to a mammalian subject, and compositions therefor, refer to the respective intact polypeptide, or any fragment or genetically engineered derivative thereof, which retains the desired biochemical function of the intact protein. Similarly, references to nucleic acids encoding anti-angiogenic polypeptides, nucleic acids encoding neuroprotective polypeptides, and other such nucleic acids for use in delivery of a gene product to a mammalian subject (which may be referred to as “transgenes” to be delivered to a recipient cell), include polynucleotides encoding the intact polypeptide or any fragment or genetically engineered derivative possessing the desired biochemical function.

An “isolated” plasmid, nucleic acid, vector, virus, virion, host cell, or other substance refers to a preparation of the substance devoid of at least some of the other components

that may also be present where the substance or a similar substance naturally occurs or is initially prepared from. Thus, for example, an isolated substance may be prepared by using a purification technique to enrich it from a source mixture. Enrichment can be measured on an absolute basis, such as weight per volume of solution, or it can be measured in relation to a second, potentially interfering substance present in the source mixture. Increasing enrichments of the embodiments of this invention are increasingly more isolated. An isolated plasmid, nucleic acid, vector, virus, host cell, or other substance is in some embodiments purified, e.g., from about 80% to about 90% pure, at least about 90% pure, at least about 95% pure, at least about 98% pure, or at least about 99%, or more, pure.

As used herein, the terms “treatment,” “treating,” and the like, refer to obtaining a desired pharmacologic and/or physiologic effect. The effect may be prophylactic in terms of completely or partially preventing a disease or symptom thereof and/or may be therapeutic in terms of a partial or complete cure for a disease and/or adverse affect attributable to the disease. “Treatment,” as used herein, covers any treatment of a disease in a mammal, particularly in a human, and includes: (a) preventing the disease from occurring in a subject which may be predisposed to the disease or at risk of acquiring the disease but has not yet been diagnosed as having it; (b) inhibiting the disease, i.e., arresting its development; and (c) relieving the disease, i.e., causing regression of the disease.

The terms “individual,” “host,” “subject,” and “patient” are used interchangeably herein, and refer to a mammal, including, but not limited to, human and non-human primates, including simians and humans; mammalian sport animals (e.g., horses, camels, etc.); mammalian farm animals (e.g., sheep, goats, cows, etc.); mammalian pets (dogs, cats, etc.); and rodents (e.g., mice, rats, etc.). In some cases, the individual is a human.

Before the present invention is further described, it is to be understood that this invention is not limited to particular embodiments described, as such may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the appended claims.

Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range and any other stated or intervening value in that stated range, is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges, and are also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the invention.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the present invention, the preferred methods and materials are now described. All publications mentioned herein are incorporated herein by reference to disclose and describe the methods and/or materials in connection with which the publications are cited.

It must be noted that as used herein and in the appended claims, the singular forms “a,” “an,” and “the” include plural

refers unless the context clearly dictates otherwise. Thus, for example, reference to “an AAV capsid” includes a plurality of such capsids and reference to “the AAV virion” includes reference to one or more AAV virions and equivalents thereof known to those skilled in the art, and so forth. It is further noted that the claims may be drafted to exclude any optional element. As such, this statement is intended to serve as antecedent basis for use of such exclusive terminology as “solely,” “only” and the like in connection with the recitation of claim elements, or use of a “negative” limitation.

It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable sub-combination. All combinations of the embodiments pertaining to the invention are specifically embraced by the present invention and are disclosed herein just as if each and every combination was individually and explicitly disclosed. In addition, all sub-combinations of the various embodiments and elements thereof are also specifically embraced by the present invention and are disclosed herein just as if each and every such sub-combination was individually and explicitly disclosed herein.

The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention. Further, the dates of publication provided may be different from the actual publication dates which may need to be independently confirmed.

#### DETAILED DESCRIPTION

The present disclosure provides recombinant adeno-associated virus (AAV) virions with altered capsid protein, where the recombinant AAV (rAAV) virions exhibit greater infectivity of a retinal cell compared to wild-type AAV; and where the rAAV virions comprise a heterologous nucleic acid. The rAAV virions exhibit greater infectivity of a retinal cell, compared to the infectivity of a corresponding wild-type AAV for the retinal cell. The retinal cell can be a photoreceptor (e.g., rods; cones), a retinal ganglion cell (RGC), a Müller cell (a Müller glial cell), an astrocyte (e.g., a retinal astrocyte), a bipolar cell, an amacrine cell, a horizontal cell, or a retinal pigment epithelium (RPE) cell. The present disclosure further provides methods of delivering a gene product to a retinal cell in an individual, and methods of treating an ocular disease. The present disclosure provides an rAAV virion with an altered capsid protein, where the rAAV virion exhibits at least 5-fold increased localization to one or more of the inner nuclear layer, the outer nuclear layer, the photoreceptor layer, the ganglion cell layer, and the retinal pigment epithelium, compared to the extent of localization to the inner nuclear layer, the outer nuclear layer, the photoreceptor layer, the ganglion cell layer, or the retinal pigment epithelium, by an AAV virion comprising the corresponding parental AAV capsid protein; and where the rAAV virions comprise a heterologous nucleic acid.

##### Variant AAV Capsid Polypeptides

The present disclosure provides a variant AAV capsid protein. A variant AAV capsid protein of the present disclosure comprises an insertion of a heterologous peptide of

from 5 amino acids to 20 amino acids in length in an insertion site in a surface-accessible (e.g., solvent-accessible) portion of a parental AAV capsid protein, such that the variant capsid protein, when present in an AAV virion, confers increased infectivity of a retinal cell compared to the infectivity of the retinal cell by an AAV virion comprising the corresponding parental AAV capsid protein. In other cases, the retinal cell is a Müller cell. Other retinal cells include amacrine cells, bipolar cells, and horizontal cells. An “insertion of from about 5 amino acids to about 20 amino acids” is also referred to herein as a “peptide insertion” (e.g., a heterologous peptide insertion). A “corresponding parental AAV capsid protein” refers to an AAV capsid protein of the same AAV serotype, without the peptide insertion. In many instances, the variant AAV capsid comprises a single heterologous peptide insert of from 5 amino acids to 20 amino acids (e.g., from 5 to 7, from 7 to 10, from 10 to 12, from 12 to 15, or from 15 to 20 amino acids) in length.

The insertion site is in the GH loop, or loop IV, of the AAV capsid protein, e.g., in a solvent-accessible portion of the GH loop, or loop IV, of the AAV capsid protein. For the GH loop/loop IV of AAV capsid, see, e.g., van Vliet et al. (2006) *Mol. Ther.* 14:809; Padron et al. (2005) *J. Virol.* 79:5047; and Shen et al. (2007) *Mol. Ther.* 15:1955. For example, the insertion site can be within amino acids 411-650 of an AAV capsid protein, as depicted in FIG. 6A-6C. For example, the insertion site can be within amino acids 570-611 of AAV2, within amino acids 571-612 of AAV1, within amino acids 560-601 of AAV5, within amino acids 571 to 612 of AAV6, within amino acids 572 to 613 of AAV7, within amino acids 573 to 614 of AAV8, within amino acids 571 to 612 of AAV9, or within amino acids 573 to 614 of AAV10, as depicted in FIG. 5. In some cases, the insertion site is between amino acids 588 and 589 of an AAV2 capsid protein, or a corresponding insertion site in an AAV of a different serotype. In some cases, the insertion site is between amino acids 587 and 588 of an AAV2 capsid protein, or a corresponding insertion site in an AAV of a different serotype.

In some cases, a heterologous peptide of from about 5 amino acids to about 20 amino acids (e.g., from 5 to 7, from 7 to 10, from 10 to 12, from 12 to 15, or from 15 to 20 amino acids) in length is inserted in an insertion site in the GH loop or loop IV of the capsid protein relative to a corresponding parental AAV capsid protein. For example, the insertion site can be between amino acids 587 and 588 of AAV2, or the corresponding positions of the capsid subunit of another AAV serotype. It should be noted that the insertion site 587/588 is based on an AAV2 capsid protein. A heterologous peptide of 5 amino acids to about 20 amino acids (e.g., from 5 to 7, from 7 to 10, from 10 to 12, from 12 to 15, or from 15 to 20 amino acids) in length can be inserted in a corresponding site in an AAV serotype other than AAV2 (e.g., AAV8, AAV9, etc.). Those skilled in the art would know, based on a comparison of the amino acid sequences of capsid proteins of various AAV serotypes, where an insertion site “corresponding to amino acids 587-588 of AAV2” would be in a capsid protein of any given AAV serotype. Sequences corresponding to amino acids 570-611 of capsid protein VP1 of AAV2 (see FIG. 4) in various AAV serotypes are shown in FIG. 5. See, e.g., GenBank Accession No. NP\_049542 for AAV1; GenBank Accession No. AAD13756 for AAV5; GenBank Accession No. AAB95459 for AAV6; GenBank Accession No. YP\_077178 for AAV7; GenBank Accession No. YP\_077180 for AAV8; GenBank Accession No. AAS99264 for AAV9 and GenBank Accession No. AAT46337 for AAV10.

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For example, the insertion site can be between amino acids 587 and 588 of AAV2, between amino acids 590 and 591 of AAV1, between amino acids 575 and 576 of AAV5, between amino acids 590 and 591 of AAV6, between amino acids 589 and 590 of AAV7, between amino acids 590 and 591 of AAV8, between amino acids 588 and 589 of AAV9, or between amino acids 588 and 589 of AAV10. The insertion sites are underlined in FIG. 5; the amino acid numbering is based on the numbering depicted in FIG. 5.

In some embodiments, a subject capsid protein includes a GH loop comprising an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to an amino acid sequence set forth in FIG. 6A-6C; and having an insertion of a heterologous peptide of from 5 to 20 amino acids (e.g., from 5 to 7, from 7 to 10, from 10 to 12, from 12 to 15, or from 15 to 20 amino acids) in length.

## Insertion Peptides

As noted above, a heterologous peptide of from about 5 amino acids to about 20 amino acids in length is inserted into the GH loop of an AAV capsid. In some cases, the insertion peptide has a length of from 5 amino acids to 20 amino acids. In some cases, the insertion peptide has a length of from 7 amino acids to 15 amino acids. In some cases, the insertion peptide has a length of from 9 amino acids to 15 amino acids. In some cases, the insertion peptide has a length of from 9 amino acids to 12 amino acids. The insertion peptide has a length of 5 amino acids, 6 amino acids, 7 amino acids, 8 amino acids, 9 amino acids, 10 amino acids, 11 amino acids, 12 amino acids, 13 amino acids, 14 amino acids, 15 amino acids, 16 amino acids, 17 amino acids, 18 amino acids, 19 amino acids, or 20 amino acids. In some cases, the insertion peptide has a length of 7 amino acids. In some cases, the insertion peptide has a length of 8 amino acids. In some cases, the insertion peptide has a length of 9 amino acids. In some cases, the insertion peptide has a length of 10 amino acids. In some cases, the insertion peptide has a length of 11 amino acids. In some cases, the insertion peptide has a length of 12 amino acids. In some cases, the insertion peptide has a length of 13 amino acids. In some cases, the insertion peptide has a length of 14 amino acids. In some cases, the insertion peptide has a length of 15 amino acids.

The peptide insert is, in some cases, a peptide of Formula I:

$$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}, \text{ where:}$$

$X_1$  is Leu, Ile, Pro, or Gln;

$X_2$  is Ala, Pro, Ser, Asp, Gly, Thr, or Val;

$X_3$  is Lys, His, Thr, Ile, Pro, Val, Arg, Ala, Asp, Glu, Asn, Gln, or Tyr;

$X_4$  (if present) is Gln, Asp, Ser, Gly, Thr, Ile, Asn, Glu, Lys, or Arg;

$X_5$  is Asp, Ser, Gln, Val, Thr, Gly, Ala, Asn, Lys, or Tyr;

$X_6$  is Thr, Ala, Gln, Ser, Glu, Pro, or Ile;

$X_7$  is Thr, Ser, Asn, Pro, Leu, Gln, Lys, Ala, or Cys;

$X_8$  is Lys, Ser, Arg, Thr, Ala, Glu, Ile, or Asn;

$X_9$  is Asn, Pro, Ser, Lys, His, Ile, Thr, or Ala; and

$X_{10}$  is Ala, Phe, Asp, Thr, Val, or Met.

Peptide inserts of Formula I include, but are not limited to, (1) LAKDATKNA (SEQ ID NO:47); (2) PAHQDTTKNA (SEQ ID NO:48); (3) LAHQDTTKNA (SEQ ID NO:49); (4) LATTSQNKPA (SEQ ID NO:50); (5) LAISDQTKHA (SEQ ID NO:51); (6) IARGVAPSSA (SEQ ID NO:52); (7) LAPDSTRSA (SEQ ID NO:53); (8) LAKGTELKPA (SEQ ID NO:54); (9) LAIIDATKNA (SEQ ID NO:55); (10) LAVD-

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GAQRSA (SEQ ID NO:56); (11) PAPQDTTKKA (SEQ ID NO:57); (12) LPHQDTTKNA (SEQ ID NO:58); (13) LAKDATKTIA (SEQ ID NO:59); (14) LAKQQSASTA (SEQ ID NO:60); (15) LAKSDQSKPA (SEQ ID NO:61); (16) LSHQDTTKNA (SEQ ID NO:62); (17) LAANQPSKPA (SEQ ID NO:63); (18) LAVSDSTKAA (SEQ ID NO:64); (19) LAAQGTAKKPA (SEQ ID NO:65); (20) LAPDQDTRNA (SEQ ID NO:66); (21) LAASDSTKAA (SEQ ID NO:67); (22) LAPQDTTKNA (SEQ ID NO:68); (23) LAKADETRPA (SEQ ID NO:69); (24) LAHQDTAKNA (SEQ ID NO:70); (25) LAHQDTKKNA (SEQ ID NO:71); (26) LAHQDTTKHA (SEQ ID NO:72); (27) LAHQDTTKKA (SEQ ID NO:73); (28) LAHQDTTRNA (SEQ ID NO:74); (29) LAHQDTTNA (SEQ ID NO:75); (30) LAHQGTTKNA (SEQ ID NO:76); (31) LAHQVTTKNA (SEQ ID NO:77); (32) LAISDQSKPA (SEQ ID NO:78); (33) LADATKTA (SEQ ID NO:79); (34) LAKDTTKNA (SEQ ID NO:80); (35) LAKSDQSRPA (SEQ ID NO:81); (36) LAPQDTKKNA (SEQ ID NO:82); (37) LATSDSTKAA (SEQ ID NO:83); (38) LAVDGSQRSA (SEQ ID NO:84); (39) LPISDQTKHA (SEQ ID NO:85); (40) LPKDATKTIA (SEQ ID NO:86); (41) LPPQDTTKNA (SEQ ID NO:87); (42) PAPQDTTKNA (SEQ ID NO:88); (43) QAHQDTTKNA (SEQ ID NO:89); (44) LAHETSPRPA (SEQ ID NO:90); (45) LAKSTSTAPA (SEQ ID NO:91); (46) LADQDTTKNA (SEQ ID NO:92); (47) LAESDQSKPA (SEQ ID NO:93); (48) LAHKDTTKNA (SEQ ID NO:94); (49) LAHKTQQKM (SEQ ID NO:95); (50) LAHQDTTENA (SEQ ID NO:96); (51) LAHQDTTINA (SEQ ID NO:97); (52) LAHQDTTKKT (SEQ ID NO:98); (53) LAHQDTTKND (SEQ ID NO:99); (54) LAHQDTTKNT (SEQ ID NO:100); (55) LAHQDTTKNV (SEQ ID NO:101); (56) LAHQDTTKTM (SEQ ID NO:102); (57) LAHQNTTKNA (SEQ ID NO:103); (58) LAHRDITTKNA (SEQ ID NO:104); (59) LAISDQTNHA (SEQ ID NO:105); (60) LAKQKSASTA (SEQ ID NO:106); (61) LAKSDQCKPA (SEQ ID NO:107); (62) LAKSDQSKPD (SEQ ID NO:108); (63) LAKSDQSNPA (SEQ ID NO:109); (64) LAKSYQSKPA (SEQ ID NO:110); (65) LANQDTTKNA (SEQ ID NO:111); (66) LAPQNTTKNA (SEQ ID NO:112); (67) LAPSSIQKPA (SEQ ID NO:113); (68) LAQQDTTKNA (SEQ ID NO:114); (69) LAYQDTTKNA (SEQ ID NO:115); (70) LDHQDTTKNA (SEQ ID NO:116); (71) LDHQDTTKSA (SEQ ID NO:117); (72) LGHQDTTKNA (SEQ ID NO:118); (73) LPHQDTTKND (SEQ ID NO:119); (74) LPHQDTTKNT (SEQ ID NO:120); (75) LPHQDTTNA (SEQ ID NO:121); (76) LTHQDTTKNA (SEQ ID NO:122); (77) LTKDATKTIA (SEQ ID NO:123); (78) LTPQDTTKNA (SEQ ID NO:124); and (79) LVHQDTTKNA (SEQ ID NO:125).

The peptide insert is, in some cases, a peptide of Formula II:

$$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}, \text{ where:}$$

$X_1$  is Leu, Ile, or Pro;

$X_2$  is Ala, Pro, or Ser;

$X_3$  is Lys, His, Thr, Ile, Pro, Val, Arg, or Ala;

$X_4$  (if present) is Gln, Asp, Ser, Gly, Thr, Ile, or Asn;

$X_5$  is Asp, Ser, Gln, Val, Thr, Gly, or Ala;

$X_6$  is Thr, Ala, Gln, Ser, Glu, or Pro;

$X_7$  is Thr, Ser, Asn, Pro, Leu, Gln, Lys, or Ala;

$X_8$  is Lys, Ser, Arg, or Thr;

$X_9$  is Asn, Pro, Ser, Lys, His, Ile, Thr, or Ala; and

$X_{10}$  is Ala.

Peptide inserts of Formula II include, but are not limited to, (1) LAKDATKNA (SEQ ID NO:47); (2) PAHQDTT-

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KNA (SEQ ID NO:48); (3) LAHQDTTKNA (SEQ ID NO:49); (4) LATTSQNKPA (SEQ ID NO:50); (5) LAIS-DQTKHA (SEQ ID NO:51); (6) IARGVAPSSA (SEQ ID NO:52); (7) LAPDSTTRSA (SEQ ID NO:53); (8) LAKGTELKPA (SEQ ID NO:54); (9) LAIIDATKNA (SEQ ID NO:55); (10) LAVDGAQRSA (SEQ ID NO:56); (11) PAPQDTTKKA (SEQ ID NO:57); (12) LPHQDTTKNA (SEQ ID NO:58); (13) LAKDATKTIA (SEQ ID NO:59); (14) LAKQQSASTA (SEQ ID NO:60); (15) LAKSDQSKPA (SEQ ID NO:61); (16) LSHQDTTKNA (SEQ ID NO:62); (17) LAANQPSKPA (SEQ ID NO:63); (18) LAVSDSTKAA (SEQ ID NO:64); (19) LAAQGTAKKPA (SEQ ID NO:65); (20) LAPDQTTRNA (SEQ ID NO:66); (21) LAASDSTKAA (SEQ ID NO:67); (22) LAPQDTTKNA (SEQ ID NO:68); (23) LAKADE-TRPA (SEQ ID NO:69); (24) LAHQDTAKNA (SEQ ID NO:70); (25) LAHQDTKKNA (SEQ ID NO:71); (26) LAHQDTTKHA (SEQ ID NO:72); (27) LAHQDTTKKA (SEQ ID NO:73); (28) LAHQDTTRNA (SEQ ID NO:74); (29) LAHQDTTNA (SEQ ID NO:75); (30) LAHQGTTKNA (SEQ ID NO:76); (31) LAHQVTTKNA (SEQ ID NO:77); (32) LAISDQSKPA (SEQ ID NO:78); (33) LADATKTA (SEQ ID NO:79); (34) LAKDTTKNA (SEQ ID NO:80); (35) LAKSDQSRPA (SEQ ID NO:81); (36) LAPQDTKKNA (SEQ ID NO:82); (37) LATSDSTKAA (SEQ ID NO:83); (38) LAVDGSQRSA (SEQ ID NO:84); (39) LPISDQTKHA (SEQ ID NO:85); (40) LPKDATKTIA (SEQ ID NO:86); (41) LPPQDTTKNA (SEQ ID NO:87); and (42) PAPQDTTKNA (SEQ ID NO:88).

Peptides of Formula H include, but are not limited to: (1) LAKDATKNA (SEQ ID NO:47); (2) PAHQDTTKNA (SEQ ID NO:48); (3) LAHQDTTKNA (SEQ ID NO:49); (4) LATTSQNKPA (SEQ ID NO:50); (5) LAISDQTKHA (SEQ ID NO:51); (6) IARGVAPSSA (SEQ ID NO:52); (7) LAPDSTTRSA (SEQ ID NO:53); (8) LAKGTELKPA (SEQ ID NO:54); (9) LAIIDATKNA (SEQ ID NO:55); (10) LAVDGAQRSA (SEQ ID NO:56); (11) PAPQDTTKKA (SEQ ID NO:57); (12) LPHQDTTKNA (SEQ ID NO:58); (13) LAKDATKTIA (SEQ ID NO:59); (14) LAKQQSASTA (SEQ ID NO:60); (15) LAKSDQSKPA (SEQ ID NO:61); (16) LSHQDTTKNA (SEQ ID NO:62); (17) LAANQPSKPA (SEQ ID NO:63); and (18) LAVSDSTKAA (SEQ ID NO:64). In some cases, the peptide insert is (1) LAKDATKNA (SEQ ID NO:47). In some cases, the peptide insert is (2) PAHQDTTKNA (SEQ ID NO:48). In some cases, the peptide insert is (3) LAHQDTTKNA (SEQ ID NO:49). In some cases, the peptide insert is (4) LATTSQNKPA (SEQ ID NO:50). In some cases, the peptide insert is (5) LAISDQTKHA (SEQ ID NO:51). In some cases, the peptide insert is (6) IARGVAPSSA (SEQ ID NO:52). In some cases, the peptide insert is (7) LAPDSTTRSA (SEQ ID NO:53). In some cases, the peptide insert is (8) LAKGTELKPA (SEQ ID NO:54). In some cases, the peptide insert is (9) LAIIDATKNA (SEQ ID NO:55). In some cases, the peptide insert is (10) LAVDGAQRSA (SEQ ID NO:56). In some cases, the peptide insert is (11) PAPQDTTKKA (SEQ ID NO:57). In some cases, the peptide insert is (12) LPHQDTTKNA (SEQ ID NO:58). In some cases, the peptide insert is (13) LAKDATKTIA (SEQ ID NO:59). In some cases, the peptide insert is (14) LAKQQSASTA (SEQ ID NO:60). In some cases, the peptide insert is (15) LAKSDQSKPA (SEQ ID NO:61). In some cases, the peptide insert is (16) LSHQDTTKNA (SEQ ID NO:62). In some cases, the peptide insert is (17) LAANQPSKPA (SEQ ID NO:63). In some cases, the peptide insert is (18) LAVSDSTKAA (SEQ ID NO:64).

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The peptide insert is, in some cases, a peptide of Formula III:

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ , where:

- 5  $X_1$  is Leu, Ile, or Pro;  
 $X_2$  is Ala, Pro, or Ser;  
 $X_3$  is Lys, His, Thr, Ile, Pro, Val, Arg, or Ala;  
 $X_4$  (if present) is Gln, Asp, Ser, Gly, Thr, Ile, or Asn;  
 $X_5$  is Asp, Ser, Gln, Val, Thr, Gly, or Ala;  
10  $X_6$  is Thr, Ala, Gln, Ser, Glu, or Pro;  
 $X_7$  is Thr, Ser, Asn, Pro, Leu, Gln, Lys, or Ala;  
 $X_8$  is Lys, Ser, Arg, or Thr;  
 $X_9$  is Asn, Pro, Ser, Lys, His, Ile, Thr, or Ala; and  
 $X_{10}$  is Ala, Thr, Asp Val, or Met.  
15 Peptide inserts of Formula III include, but are not limited to, (1) LAKDATKNA (SEQ ID NO:47); (2) PAHQDTTKNA (SEQ ID NO:48); (3) LAHQDTTKNA (SEQ ID NO:49); (6) IARGVAPSSA (SEQ ID NO:52); (7) LAPDSTRSA (SEQ ID NO:53); (8) LAKGTELKPA (SEQ ID NO:54); (9) LAIIDATKNA (SEQ ID NO:55); (10) LAVDGAQRSA (SEQ ID NO:56); (11) PAPQDTTKKA (SEQ ID NO:57); (12) LPHQDTTKNA (SEQ ID NO:58); (13) LAKDATKTIA (SEQ ID NO:59); (14) LAKQQSASTA (SEQ ID NO:60); (16) LSHQDTTKNA (SEQ ID NO:62); (17) LAANQPSKPA (SEQ ID NO:63); (18) LAVSDSTKAA (SEQ ID NO:64); (19) LAAQGTAKPA (SEQ ID NO:65); (20) LAPDQTTRNA (SEQ ID NO:66); (24) LAHQDTAKNA (SEQ ID NO:70); (25) LAHQDTKKNA (SEQ ID NO:71); (26) LAHQDTTKHA (SEQ ID NO:72); (27) LAHQDTTKKA (SEQ ID NO:73); (28) LAHQDTTRNA (SEQ ID NO:74); (29) LAHQDTTNA (SEQ ID NO:75); (30) LAHQGTTKNA (SEQ ID NO:76); (21) LAASDSTKAA (SEQ ID NO:67); (22) LAPQDTTKNA (SEQ ID NO:68); (31) LAHQVTTKNA (SEQ ID NO:77); (33) LAKDATKTA (SEQ ID NO:79); (34) LAKDTTKNA (SEQ ID NO:80); (36) LAPQDTKKNA (SEQ ID NO:82); (37) LATSDSTKAA (SEQ ID NO:83); (38) LAVDGSQRSA (SEQ ID NO:84); (41) LPPQDTTKNA (SEQ ID NO:87); (42) PAPQDTTKNA (SEQ ID NO:88); (52) LAHQDTTKKT (SEQ ID NO:98); (53) LAHQDTTKND (SEQ ID NO:99); (54) LAHQDTTKNT (SEQ ID NO:100); (55) LAHQDTTKNV (SEQ ID NO:101); (56) LAHQDTTKTM (SEQ ID NO:102); (73) LPHQDTTKND (SEQ ID NO:119); and (74) LPHQDTTKNT (SEQ ID NO:120).

The peptide insert is, in some cases, a peptide of Formula IV:

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ , where:

- 50  $X_1$  is Leu;  
 $X_2$  is Ala;  
 $X_3$  is Lys, His, Thr, Ile, Pro, or Val;  
 $X_4$  (if present) is Gln, Asp, Ser, or Gly;  
 $X_5$  is Asp, Ser, or Gln;  
55  $X_6$  is Thr, Ala, Gln, or Ser;  
 $X_7$  is Thr or Ser;  
 $X_8$  is Lys, Ser, or Arg;  
 $X_9$  is Asn, Pro, or Ser; and  
 $X_{10}$  is Ala.  
60 Peptide inserts of Formula IV include, but are not limited to, (1) LAKDATKNA (SEQ ID NO:47); (3) LAHQDTTKNA (SEQ ID NO:49); (7) LAPDSTTRSA (SEQ ID NO:53); (15) LAKSDQSKPA (SEQ ID NO:61); (20) LAPDQTTRNA (SEQ ID NO:66); (22) LAPQDTTKNA (SEQ ID NO:68); (28) LAHQDTTRNA (SEQ ID NO:74); (32) LAISDQSKPA (SEQ ID NO:78); (34) LAKDTTKNA (SEQ ID NO:80); and (35) LAKSDQSRPA (SEQ ID NO:81).



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The peptide insert is, in some cases, a peptide of Formula V:

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ , where:

- $X_1$  is Leu;
- $X_2$  is Ala;
- $X_3$  is Lys or His;
- $X_4$  (if present) is Gln, Asp, Ser, or Gly;
- $X_5$  is Asp, Ser, or Gln;
- $X_6$  is Thr, Ala, Gln, or Ser;
- $X_7$  is Thr or Ser;
- $X_8$  is Lys, Ser, or Arg;
- $X_9$  is Asn, Pro, or Ser; and
- $X_{10}$  is Ala.

Peptide inserts of Formula V include, but are not limited to, (1) LAKDATKNA (SEQ ID NO:47); (15) LAKSDQSKPA (SEQ ID NO:51); (34) LAKDTTKNA (SEQ ID NO:80); and (35) LAKSDQSRPA (SEQ ID NO:81).

The peptide insert is, in some cases, a peptide of Formula VI:

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ , where:

- $X_1$  is Leu;
- $X_2$  is Ala;
- $X_3$  is Asn, Lys, Thr, Gln, Ser, Ile, or Leu;
- $X_4$  is Ser, Ala, Thr, Glu, Gln, Gly, Lys, or Pro;
- $X_5$  is Asp, Pro, Glu, Thr, Asn, or Arg;
- $X_6$  is Ile, His, Thr, Gln, Asn, Tyr, Asp, or Glu;
- $X_7$  is Gln, Thr, Asn, Ala, or Lys;
- $X_8$  is Lys, Thr, Arg, or Asp;
- $X_9$  is Pro, Asn, Thr, Arg, Lys, or Ser; and
- $X_{10}$  is Ala.

Peptides of Formula VI include, but are not limited to: (80) LAKANQNTPA (SEQ ID NO:126); (81) LATT-PITKPA (SEQ ID NO:127); (82) LATTPIAKPA (SEQ ID NO:128); (83) LAIEDHTKSA (SEQ ID NO:129); (84) LAQSEHQRPA (SEQ ID NO:130); (85) LAKSPNKDNA (SEQ ID NO:131); (86) LANQDYTKTA (SEQ ID NO:132); (87) LANSTDQTRA (SEQ ID NO:133); (88) LALGETTRPA (SEQ ID NO:134); (89) LANSTEQTRA (SEQ ID NO:135); (90) LAQADTTKNA (SEQ ID NO:136); (91) LASKDITKTA (SEQ ID NO:137); and (92) LASPRHNKCC (SEQ ID NO:138).

In some cases, the peptide insert is a peptide of Formula VII: LAHQDTTKX<sub>1</sub>X<sub>2</sub>X<sub>3</sub> (SEQ ID NO:148), where  $X_1$  is Lys, Thr, Asn, or His;  $X_2$  is Ala, Thr, Val, Ile, Met, or Asp; and  $X_3$ , if present, is Ala. Peptides of Formula VII include, but are not limited to: (26) LAHQDTTKHA (SEQ ID NO:72); (27) LAHQDTTKKA (SEQ ID NO:73); (52) LAHQDTTKKT (SEQ ID NO:98); (53) LAHQDTTKND (SEQ ID NO:99); (54) LAHQDTTKNT (SEQ ID NO:100); (55) LAHQDTTKNV (SEQ ID NO:101); (56) LAHQDTTKTM (SEQ ID NO:102); and (93) LAHQDTTKTIA (SEQ ID NO:139).

In some cases, the peptide insert is a peptide of Formula VIII: LAX<sub>1</sub>QX<sub>2</sub>TX<sub>3</sub>X<sub>4</sub>X<sub>5</sub>X<sub>6</sub> (SEQ ID NO:149), where  $X_1$  is Ala, Pro, Asp, or His;  $X_2$  is Gly or Asp;  $X_3$  is Ala, Thr, or Lys;  $X_4$  is Asn, Glu, Lys, Arg, or Thr;  $X_5$  is Leu, Asn, Lys, or Thr; and  $X_6$ , if present, is Ala, Thr, Asp, Val, or Met. Peptides of Formula VIII include, but are not limited to, (94) LAAQGTANL (SEQ ID NO:140); (22) LAPQDTTKNA (SEQ ID NO:68); (46) LADQDTTKNA (SEQ ID NO:92); (24) LAHQDTAKNA (SEQ ID NO:70); (25) LAHQDTK-KNA (SEQ ID NO:71); (26) LAHQDTTKHA (SEQ ID NO:72); (27) LAHQDTTKKA (SEQ ID NO:73); (28) LAHQDTTRNA (SEQ ID NO:74); (29) LAHQDTTNA

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(SEQ ID NO:75); (50) LAHQDTTENA (SEQ ID NO:96); (51) LAHQDTTINA (SEQ ID NO:97); (52) LAHQDTTKKT (SEQ ID NO:98); (53) LAHQDTTKND (SEQ ID NO:99); (54) LAHQDTTKNT (SEQ ID NO:100); (55) LAHQDTTKNV (SEQ ID NO:101); and (56) LAHQDTTKTM (SEQ ID NO:102).

In some cases, the peptide insert is a peptide of Formula IX: X<sub>1</sub>AX<sub>2</sub>X<sub>3</sub>DX<sub>4</sub>TKX<sub>5</sub>A (SEQ ID NO:150), where  $X_1$  is Val or Leu;  $X_2$  is Ile, Val, His, or Asp;  $X_3$  is Glu, Ser, Lys, or Gln;  $X_4$  is His, Ser, or Thr; and  $X_5$  is Ser, Ala, Asn, His, or Lys. Peptides of Formula IX include, but are not limited to, (95) VAIEDHTKSA (SEQ ID NO:141); (18) LAVSD-STKAA (SEQ ID NO:64); (46) LADQDTTKNA (SEQ ID NO:92); (48) LAHKDTTKNA (SEQ ID NO:94); (26) LAHQDTTKHA (SEQ ID NO:72); and (27) LAHQDTTKKA (SEQ ID NO:73).

In some cases, the peptide insert is a peptide of Formula X: X<sub>1</sub>X<sub>2</sub>X<sub>3</sub>AX<sub>4</sub>QX<sub>5</sub>TX<sub>6</sub>KNA (SEQ ID NO:151), where  $X_1$ , if present, is Leu;  $X_2$ , if present, is Ala;  $X_3$  is Lys, Leu, or Pro;  $X_4$  is Asn, His, Pro, or Tyr;  $X_5$  is Asn, Gly, Val, or Asp; and  $X_6$  is Pro or Thr. Peptides of Formula X include, but are not limited to, (96) LAKANQNTPKNA (SEQ ID NO:142); (57) LAHQNTTKNA (SEQ ID NO:103); (66) LAPQNTT-KNA (SEQ ID NO:112); (69) LAYQDTTKNA (SEQ ID NO: 115); (30) LAHQGTTKNA (SEQ ID NO:76); (31) LAHQVTTKNA (SEQ ID NO:77); and (42) PAPQDTT-KNA (SEQ ID NO:88).

In some cases, the peptide insert is LAHQDTTKKX (SEQ ID NO:143), where X is any amino acid. In some cases, the peptide insert is LAHQDTTKKX (SEQ ID NO:143), where X is Ala, Thr, Asp, Val, or Met. In some cases, the peptide insert is (27) LAHQDTTKKA (SEQ ID NO:73). In some cases, the peptide insert is (52) LAHQDTTKKT (SEQ ID NO:98). In some cases, the peptide insert is LAHQDTTKKD (SEQ ID NO:144). In some cases, the peptide insert is LAHQDTTKKV (SEQ ID NO:145). In some cases, the peptide insert is LAHQDTTKKM (SEQ ID NO:146).

In some cases, the peptide insert is not (88) LAL-GETTRPA (SEQ ID NO:134). In some cases, the peptide insert is not LGETTRP (SEQ ID NO:147).

Suitable peptide inserts include, but are not limited to, (1) LAKDATKNA (SEQ ID NO:47); (2) PAHQDTTKNA (SEQ ID NO:48); (3) LAHQDTTKNA (SEQ ID NO:49); (4) LATTSQNKPA (SEQ ID NO:50); (5) LAISDQTKHA (SEQ ID NO:51); (6) IARGVAPSSA (SEQ ID NO:52); (7) LAP-DSTTRSA (SEQ ID NO:53); (8) LAKGTELKPA (SEQ ID NO:54); (9) LAIIDATKNA (SEQ ID NO:55); (10) LAVD-GAQRSA (SEQ ID NO:56); (11) PAPQDTTKKA (SEQ ID NO:57); (12) LPHQDTTKNA (SEQ ID NO:58); (13) LAK-DATKTIA (SEQ ID NO:59); (14) LAKQQSASTA (SEQ ID NO:60); (15) LAKSDQSKPA (SEQ ID NO:61); (16) LSHQDTTKNA (SEQ ID NO:62); (17) LAANQPSKPA (SEQ ID NO:63); (18) LAVSDSTKAA (SEQ ID NO:64); (19) LAAQGTAKKPA (SEQ ID NO:65); (20) LAPDQT-TRNA (SEQ ID NO:66); (21) LAASDSTKAA (SEQ ID NO:67); (22) LAPQDTTKNA (SEQ ID NO:68); (23) LAKADETRPA (SEQ ID NO:69); (24) LAHQDTAKNA (SEQ ID NO:70); (25) LAHQDTTKNA (SEQ ID NO:71); (26) LAHQDTTKHA (SEQ ID NO:72); (27) LAHQDTTKKA (SEQ ID NO:73); (28) LAHQDTTRNA (SEQ ID NO:74); (29) LAHQDTTNA (SEQ ID NO:75); (30) LAHQGTTKNA (SEQ ID NO:76); (31) LAHQVTT-KNA (SEQ ID NO:77); (32) LAISDQSKPA (SEQ ID NO:78); (33) LADATKTA (SEQ ID NO:79); (34) LAK-DATTKNA (SEQ ID NO:80); (35) LAKSDQSRPA (SEQ ID NO:81); (36) LAPQDTTKNA (SEQ ID NO:82); (37)

LATSDSTKAA (SEQ ID NO:83); (38) LAVDGSQRSA (SEQ ID NO:84); (39) LPISDQTKHA (SEQ ID NO:85); (40) LPKDATKTIA (SEQ ID NO:86); (41) LPPQDTTKNA (SEQ ID NO:87); (42) PAPQDTTKNA (SEQ ID NO:88); (43) QAHQDTTKNA (SEQ ID NO:89); (44) LAHET-  
 5 SPRPA (SEQ ID NO:90); (45) LAKSTSTAPA (SEQ ID NO:91); (46) LADQDTTKNA (SEQ ID NO:92); (47) LAESDQSKPA (SEQ ID NO:93); (48) LAHKDTTKNA (SEQ ID NO:94); (49) LAHKTQQKM (SEQ ID NO:95); (50) LAHQDTTENA (SEQ ID NO:96); (51) LAHQDT-  
 10 TINA (SEQ ID NO:97); (52) LAHQDTTKKT (SEQ ID NO:98); (53) LAHQDTTKND (SEQ ID NO:99); (54) LAHQDTTKNT (SEQ ID NO:100); (55) LAHQDTTKNV (SEQ ID NO:101); (56) LAHQDTTKTM (SEQ ID NO:102); (57) LAHQNTTKNA (SEQ ID NO:103); (58) LAHRD  
 15 TTKNA (SEQ ID NO:104); (59) LAISDQTNHA (SEQ ID NO:105); (60) LAKQKSASTA (SEQ ID NO:106); (61) LAKSDQCKPA (SEQ ID NO:107); (62) LAKSDQSKPD (SEQ ID NO:108); (63) LAKSDQSNPA (SEQ ID NO:109); (64) LAKSYQSKPA (SEQ ID NO:110); (65) LANQDTTKNA (SEQ ID NO:111); (66) LAPQNTT-  
 20 KNA (SEQ ID NO:112); (67) LAPSSIQKPA (SEQ ID NO:113); (68) LAQQDTTKNA (SEQ ID NO:114); (69) LAYQDTTKNA (SEQ ID NO: 115); (70) LDHQDTTKNA (SEQ ID NO: 116); (71) LDHQDTTKSA (SEQ ID NO: 117); (72) LGHQDTTKNA (SEQ ID NO: 118); (73) LPHQDTTKND (SEQ ID NO:119); (74) LPHQDTTKNT (SEQ ID NO:120); (75) LPHQDTTNNNA (SEQ ID NO:121); (76) LTHQDTTKNA (SEQ ID NO:122); (77) LTKDATK-  
 25 TIA (SEQ ID NO:123); (78) LTPQDTTKNA (SEQ ID NO:124); (79) LVHQDTTKNA (SEQ ID NO:125); (80) LAKANQNTPA (SEQ ID NO:126); (81) LATTPIKPA (SEQ ID NO:127); (82) LATTPIAKPA (SEQ ID NO:128); (83) LAIEDHTKSA (SEQ ID NO:129); (84) LAQSEHQ  
 30 RPA (SEQ ID NO:130); (85) LAKSPNKDNA (SEQ ID NO:131); (86) LANQDYTKTA (SEQ ID NO:132); (87) LANSTDQTRA (SEQ ID NO:133); (88) LALGETTRPA (SEQ ID NO:134); (89) LANSTEQTRA (SEQ ID NO:135); (90) LAQADTTKNA (SEQ ID NO:136); (91) LASKDITKTA (SEQ ID NO:137); (92) LASPRHNKCC (SEQ ID NO:138); (93) LAHQDTTKTIA (SEQ ID NO:139); (94) LAAQGTANL (SEQ ID NO:140); (95) VAIEDHTKSA (SEQ ID NO:141); and (96) LAKANQNTPKNA (SEQ ID NO:142).

In some cases, the peptide insert is (11) PAPQDTTKKA (SEQ ID NO:57). In some cases, the peptide insert is (7) LAPDSTTRSA (SEQ ID NO:53).

In some embodiments, a subject rAAV virion capsid does not include any other amino acid substitutions, insertions, or deletions, other than an insertion of from about 5 amino acids to about 20 amino acids (e.g., 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids; e.g., 9 amino acids, 10 amino acids, 11 amino acids, or 12 amino acids) in the GH loop or loop IV relative to a corresponding parental AAV capsid protein. In other embodiments, a subject rAAV virion capsid includes from 1 to about 25 amino acid insertions, deletions, or substitutions, compared to the parental AAV capsid protein, in addition to an insertion of from about 5 amino acids to about 20 amino acids (e.g., 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids; e.g., 9 amino acids, 10 amino acids, 11 amino acids, or 12 amino acids) in the GH loop or loop IV relative to a corresponding parental AAV capsid protein. For example, in some embodiments, a subject rAAV virion capsid includes from 1 to about 5, from about 5 to about 10, from about 10 to about 15, from about 15 to about 20, or from about 20 to about 25 amino acid insertions, deletions, or substitutions,

compared to the parental AAV capsid protein, in addition to an insertion of from about 5 amino acids to about 20 amino acids (e.g., 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids; e.g., 9 amino acids, 10 amino acids, 11 amino acids, or 12 amino acids) in the GH loop or loop IV relative to a corresponding parental AAV capsid protein.

In some cases, a subject rAAV virion capsid does not include one, two, three, or four, of the following amino acid substitutions: Y273F, Y444F, Y500F, and Y730F.

In some cases, a subject variant capsid polypeptide comprises, in addition to an insertion peptide as described above, one, two, three, or four, of the following amino acid substitutions: Y273F, Y444F, Y500F, and Y730F.

In some cases, a subject rAAV virion capsid is a chimeric capsid, e.g., the capsid comprises a portion of an AAV capsid of a first AAV serotype and a portion of an AAV capsid of a second serotype; and comprises an insertion of from about 5 amino acids to about 20 amino acids (e.g., 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids; e.g., 9 amino acids, 10 amino acids, 11 amino acids, or 12 amino acids) in the GH loop or loop IV relative to a corresponding parental AAV capsid protein.

In some embodiments, a subject rAAV virion comprises a capsid protein comprising an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, amino acid sequence identity to the amino acid sequence provided in FIG. 4; and an insertion of from about 5 amino acids to about 20 amino acids (e.g., 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids; e.g., 9 amino acids, 10 amino acids, 11 amino acids, or 12 amino acids) in the GH loop or loop IV relative to a corresponding parental AAV capsid protein. In some embodiments, a subject rAAV virion comprises a capsid protein comprising an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, amino acid sequence identity to the amino acid sequence provided in FIG. 4; and an insertion of from about 5 amino acids to about 20 amino acids (e.g., 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids; e.g., 9 amino acids, 10 amino acids, 11 amino acids, or 12 amino acids) between amino acids 587 and 588 relative to the amino acid sequence depicted in FIG. 4, or at a corresponding site relative to a corresponding parental AAV capsid protein.

In some embodiments, a subject rAAV virion comprises a capsid protein that includes a GH loop comprising an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to an amino acid sequence set forth in FIG. 5, and comprising an insertion of from about 5 amino acids to about 20 amino acids (e.g., 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids; e.g., 9 amino acids, 10 amino acids, 11 amino acids, or 12 amino acids) between the bolded and underlined amino acids.

In some embodiments, a subject rAAV virion comprises a capsid protein comprising an amino acid sequence having at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%, amino acid sequence identity to any one of the amino acid sequences provided in FIG. 6A-6C; and an insertion of from about 5 amino acids to about 20 amino acids (e.g., 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids; e.g., 9 amino acids, 10 amino acids, 11 amino acids, or 12 amino acids) between amino acids 587 and 588 of AAV2, or at a corresponding site



increased ability to cross the internal limiting membrane (ILM), compared to the ability of an AAV virion comprising the corresponding parental AAV capsid protein to cross the ILM.

In some cases, a subject rAAV virion exhibits at least 5-fold, at least 10-fold, at least 15-fold, at least 20-fold, at least 25-fold, at least 50-fold, or more than 50-fold, increased ability, when administered via intravitreal injection, to cross the ILM, compared to the ability of an AAV virion comprising the corresponding parental AAV capsid protein to cross the ILM when administered via intravitreal injection.

A subject rAAV virion can cross the ILM, and can also traverse cell layers, including Miller cells, amacrine cells, etc., to reach the photoreceptor cells and or RPE cells. For example, a subject rAAV virion, when administered via intravitreal injection, can cross the ILM, and can also traverse cell layers, including Müller cells, amacrine cells, etc., to reach the photoreceptor cells and or RPE cells.

In some cases, a subject rAAV virion, when injected intravitreally, exhibits at least 5-fold, at least 10-fold, at least 15-fold, at least 20-fold, at least 25-fold, at least 50-fold, or more than 50-fold, increased localization past the ILM, compared to the extent of localization past the ILM by an intravitreally injected control AAV virion comprising the corresponding parental AAV capsid protein. For example, in some cases, a subject rAAV virion, when injected intravitreally, exhibits at least 5-fold, at least 10-fold, at least 15-fold, at least 20-fold, at least 25-fold, at least 50-fold, or more than 50-fold, increased localization to the retinal pigment epithelium (RPE), compared to the extent of localization to the RPE layer by an intravitreally injected control AAV virion comprising the corresponding parental AAV capsid protein. As another example, in some cases, a subject rAAV virion, when injected intravitreally, exhibits at least 5-fold, at least 10-fold, at least 15-fold, at least 20-fold, at least 25-fold, at least 50-fold, or more than 50-fold, increased localization to the photoreceptor (PR) layer, compared to the extent of localization to the PR layer by an intravitreally injected control AAV virion comprising the corresponding parental AAV capsid protein. As another example, in some cases, a subject rAAV virion, when injected intravitreally, exhibits at least 5-fold, at least 10-fold, at least 15-fold, at least 20-fold, at least 25-fold, at least 50-fold, or more than 50-fold, increased localization to the inner nuclear layer, compared to the extent of localization to the inner nuclear layer by an intravitreally injected control AAV virion comprising the corresponding parental AAV capsid protein. As another example, in some cases, a subject rAAV virion, when injected intravitreally, exhibits at least 5-fold, at least 10-fold, at least 15-fold, at least 20-fold, at least 25-fold, at least 50-fold, or more than 50-fold, increased localization to the outer nuclear layer, compared to the extent of localization to the outer nuclear layer by an intravitreally injected control AAV virion comprising the corresponding parental AAV capsid protein. As another example, in some cases, a subject rAAV virion, when injected intravitreally, exhibits at least 5-fold, at least 10-fold, at least 15-fold, at least 20-fold, at least 25-fold, at least 50-fold, or more than 50-fold, increased localization to the ganglion cell layer, compared to the extent of localization to the ganglion cell layer by an intravitreally injected control AAV virion comprising the corresponding parental AAV capsid protein.

In some embodiments, a subject rAAV virion selectively infects a retinal cell, e.g., a subject rAAV virion infects a retinal cell with 10-fold, 15-fold, 20-fold, 25-fold, 50-fold,

or more than 50-fold, specificity than a non-retinal cell, e.g., a cell outside the eye. For example, in some embodiments, a subject rAAV virion selectively infects a retinal cell, e.g., a subject rAAV virion infects a photoreceptor cell with 10-fold, 15-fold, 20-fold, 25-fold, 50-fold, or more than 50-fold, specificity than a non-retinal cell, e.g., a cell outside the eye.

In some embodiments, a subject rAAV virion selectively infects a photoreceptor cell, e.g., a subject rAAV virion infects a photoreceptor cell with 10-fold, 15-fold, 20-fold, 25-fold, 50-fold, or more than 50-fold, specificity than a non-photoreceptor cell present in the eye, e.g., a retinal ganglion cell, a Miller cell, etc.

In some embodiments, a subject rAAV virion exhibits at least 10-fold, at least 15-fold, at least 20-fold, at least 25-fold, at least 50-fold, or more than 50-fold, increased infectivity of a photoreceptor cell, when administered via intravitreal injection, compared to the infectivity of the photoreceptor cell by an AAV virion comprising the corresponding parental AAV capsid protein, when administered via intravitreal injection.

#### Gene Products

A subject rAAV virion comprises a heterologous nucleic acid comprising a nucleotide sequence encoding a gene product (a heterologous gene product. In some cases, the gene product is a polypeptide. In some cases, the gene product is an RNA. Where the gene product is an RNA, in some cases, the RNA gene product encodes a polypeptide. In some cases, an rAAV virion of the present disclosure comprises a single heterologous nucleic acid comprising a nucleotide sequence encoding a single heterologous gene product. In some cases, an rAAV virion of the present disclosure comprises a single heterologous nucleic acid comprising a nucleotide sequence encoding two heterologous gene products. In some cases, an rAAV virion of the present disclosure comprises two heterologous nucleic acids, each comprising a nucleotide sequence encoding a heterologous gene product.

In some embodiments, the gene product is an interfering RNA. In some embodiments, the gene product is an aptamer. In some embodiments, the gene product is a polypeptide. In some embodiments, the gene product is a site-specific nuclease that provide for site-specific knock-down of gene function. In some embodiments, the gene product is an RNA-guided endonuclease that provides for modification of a target nucleic acid.

#### Interfering RNA

Where the gene product is an interfering RNA (RNAi), suitable RNAi include RNAi that decrease the level of an apoptotic or angiogenic factor in a cell. For example, an RNAi can be an shRNA or siRNA that reduces the level of a gene product that induces or promotes apoptosis in a cell. Genes whose gene products induce or promote apoptosis are referred to herein as “pro-apoptotic genes” and the products of those genes (mRNA; protein) are referred to as “pro-apoptotic gene products.” Pro-apoptotic gene products include, e.g., Bax, Bid, Bak, and Bad gene products. See, e.g., U.S. Pat. No. 7,846,730.

Interfering RNAs could also be against an angiogenic product, for example vascular endothelial growth factor (VEGF) (e.g., Cand5; see, e.g., U.S. Patent Publication No. 2011/0143400; U.S. Patent Publication No. 2008/0188437; and Reich et al. (2003) *Mol. Vis.* 9:210); VEGF receptor-1 (VEGFR1) (e.g., Sirna-027; see, e.g., Kaiser et al. (2010) *Am. J. Ophthalmol.* 150:33; and Shen et al. (2006) *Gene Ther.* 13:225); or VEGF receptor-2 (VEGFR2) (Kou et al.

(2005) *Biochem.* 44:15064). See also, U.S. Pat. Nos. 6,649,596, 6,399,586, 5,661,135, 5,639,872, and 5,639,736; and 7,947,659 and 7,919,473.

#### Aptamers

Where the gene product is an aptamer, exemplary aptamers of interest include an aptamer against VEGF. See, e.g., Ng et al. (2006) *Nat. Rev. Drug Discovery* 5:123; and Lee et al. (2005) *Proc. Natl. Acad. Sci. USA* 102:18902. For example, a VEGF aptamer can comprise the nucleotide sequence 5'-cgcaaucagugaaugcuuauacaucg-3' (SEQ ID NO:11). Also suitable for use is a platelet-derived growth factor (PDGF)-specific aptamer, e.g., E10030; see, e.g., Ni and Hui (2009) *Ophthalmologica* 223:401; and Akiyama et al. (2006) *J. Cell Physiol.* 207:407).

#### Polypeptides

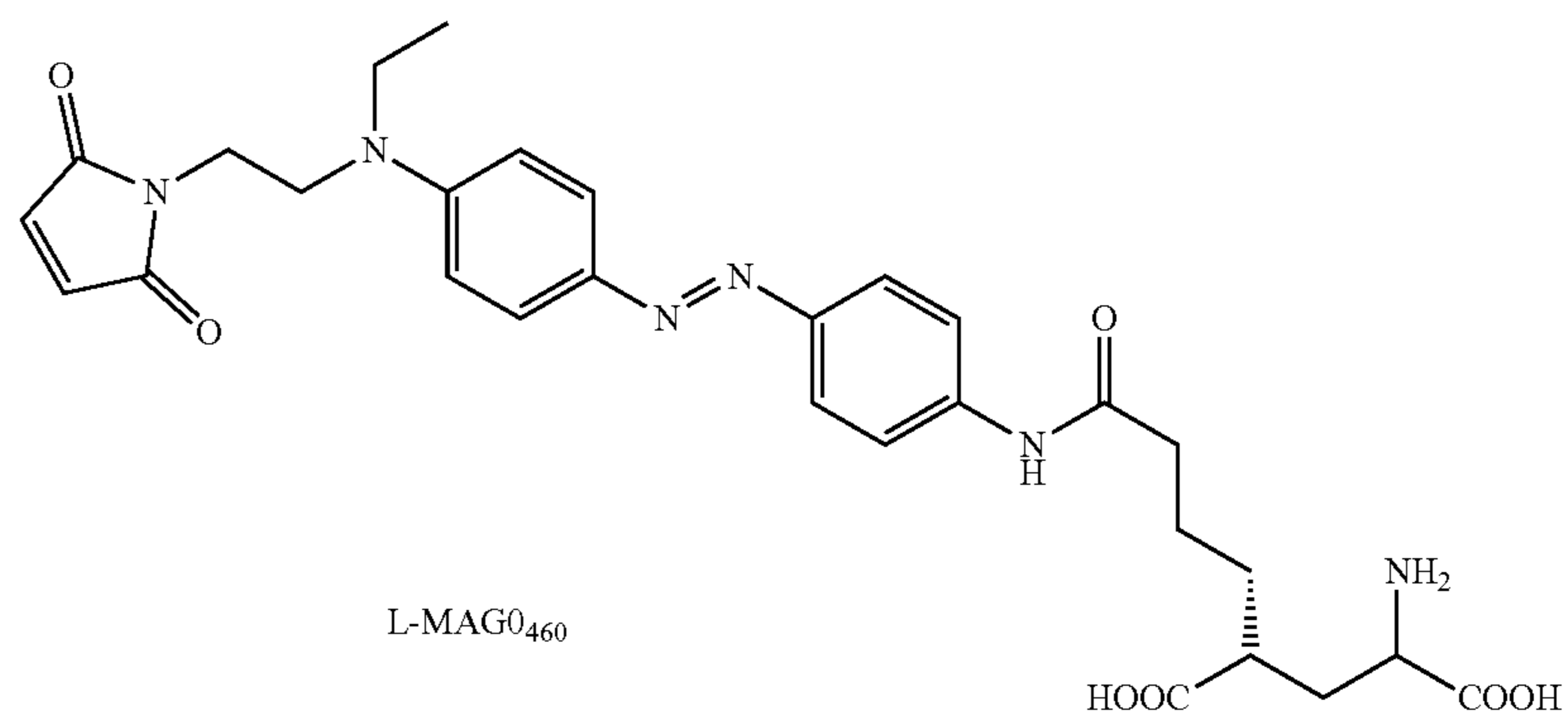
Where the gene product is a polypeptide, the polypeptide is generally a polypeptide that enhances function of a retinal cell, e.g., the function of a rod or cone photoreceptor cell, a retinal ganglion cell, a Müller cell, a bipolar cell, an amacrine cell, a horizontal cell, or a retinal pigment epithelial cell. Exemplary polypeptides include neuroprotective polypeptides (e.g., glial cell derived neurotrophic factor (GDNF), ciliary neurotrophic factor (CNTF), neurotro-

phin-4 (NT4), nerve growth factor (NGF), and neurturin (NTN)); anti-angiogenic polypeptides (e.g., a soluble VEGF receptor; a VEGF-binding antibody; a VEGF-binding antibody fragment (e.g., a single chain anti-VEGF antibody); endostatin; tumstatin; angiostatin; a soluble Flt polypeptide (Lai et al. (2005) *Mol. Ther.* 12:659); an Fc fusion protein comprising a soluble Flt polypeptide (see, e.g., Pechan et al. (2009) *Gene Ther.* 16:10); pigment epithelium-derived factor (PEDF); a soluble Tie-2 receptor; etc.); tissue inhibitor of metalloproteinases-3 (TIMP-3); a light-responsive opsin, e.g., a rhodopsin; anti-apoptotic polypeptides (e.g., Bcl-2, Bcl-XL; XIAP); and the like. Suitable polypeptides include, but are not limited to, glial derived neurotrophic factor (GDNF); fibroblast growth factor; fibroblast growth factor 2; neurturin (NTN); ciliary neurotrophic factor (CNTF); nerve growth factor (NGF); neurotrophin-4 (NT4); brain derived neurotrophic factor (BDNF; e.g., a polypeptide comprising an amino acid sequence having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to a contiguous stretch of from about 200 amino acids to 247 amino acids of the amino acid sequence depicted in FIG. 7B (SEQ ID NO:11)); epidermal growth factor; rhodopsin; X-linked inhibitor of apoptosis; and Sonic hedgehog.

Suitable light-responsive opsins include, e.g., a light-responsive opsin as described in U.S. Patent Publication No.

2007/0261127 (e.g., channelrhodopsin-2; ChR2; Chop2); U.S. Patent Publication No. 2001/0086421; U.S. Patent Publication No. 2010/0015095; U.S. Patent Publication No. 2016/0002302; U.S. Patent Publication No. 2013/0347137; U.S. Patent Publication No. 2013/0019325; and Diester et al. (2011) *Nat. Neurosci.* 14:387. See, Thyagarajan et al. (2010) *J. Neurosci.* 30(26):8745-8758; Lagali et al. (2008) *Nat. Neurosci.* 11(6):667-675; Doroudchi et al. (2011) *Mol. Ther.* 19(7):1220-1229; Henriksen et al. (2014) *J. Ophthalmic Vis. Res.* 9:374; Tomita et al. (2014) *Mol. Ther.* 22:1434.

Suitable polypeptides include light-gated ion channel polypeptides. See, e.g., Gaub et al. (2014) *Proc. Natl. Acad. Sci. USA* 111:E5574. For example, a suitable polypeptide is a light-gated ionotropic glutamate receptor (LiGluR). Expression of LiGluR in retinal ganglion cells and ON-bipolar cells, in the presence of a photoisomerizable compound, renders the cells responsive to light. LiGluR comprises a L439C substitution; see, Caporale et al. (2011) *Mol. Ther.* 19:1212-1219; Volgraf et al. (2006) *Nat Chem Biol.* 2:47-52; and Gorostiza et al. (2007) *Proc Natl Acad Sci USA.* 104:10865-10870. Photoisomerizable compounds include, e.g., maleimide-azobenzene-glutamate 0 with peak efficiency at 460 nm (MAG0<sub>460</sub>). MAG0<sub>460</sub> has the following structure:



Suitable polypeptides also include retinoschisin (e.g., a polypeptide comprising an amino acid sequence having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to a contiguous stretch of from about 200 amino acids to 224 amino acids of the amino acid sequence depicted in FIG. 7A (SEQ ID NO:10). Suitable polypeptides include, e.g., retinitis pigmentosa GTPase regulator (RPGR)-interacting protein-1 (see, e.g., GenBank Accession Nos. Q96KN7, Q9EPQ2, and Q9GLM3) (e.g., a polypeptide comprising an amino acid sequence having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to a contiguous stretch of from about 1150 amino acids to about 1200 amino acids, or from about 1200 amino acids to 1286 amino acids, of the amino acid sequence depicted in FIG. 7F (SEQ ID NO:15); peripherin-2 (Prph2) (see, e.g., GenBank Accession No. NP\_000313 (e.g., a polypeptide comprising an amino acid sequence having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to a contiguous stretch of from about 300 amino acids to 346 amino acids of the amino acid sequence depicted in FIG. 7D (SEQ ID NO:13); and Travis et al. (1991) *Genomics* 10:733); peripherin (e.g., a polypeptide comprising an amino acid sequence having at least about 90%, at least about 95%, at least about 98%, at least about

99%, or 100%, amino acid sequence identity to a contiguous stretch of from about 400 amino acids to about 470 amino acids of the amino acid sequence depicted in FIG. 7E (SEQ ID NO:14); a retinal pigment epithelium-specific protein (RPE65), (e.g., a polypeptide comprising an amino acid sequence having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to a contiguous stretch of from about 200 amino acids to 247 amino acids of the amino acid sequence depicted in FIG. 7C (SEQ ID NO:12)) (see, e.g., GenBank AAC39660; and Morimura et al. (1998) *Proc. Natl. Acad. Sci. USA* 95:3088); rod-derived cone viability factor (RdCVF) (e.g., a polypeptide comprising an amino acid sequence having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence depicted in any one of FIGS. 7H, 7I, and 7J; choroideremia (e.g., a polypeptide comprising an amino acid sequence having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence depicted in FIG. 7G); retinitis pigmentosa GTPase regulator (RPGR) (e.g., a polypeptide comprising an amino acid sequence having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence depicted in one of FIG. 7S-7V); and the like. For example, in some cases, a suitable RPGR polypeptide comprises an amino acid sequence having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence depicted in FIG. 7S. As another example, in some cases, a suitable RPGR polypeptide comprises an amino acid sequence having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence depicted in FIG. 7T. example, in some cases, a suitable RPGR polypeptide comprises an amino acid sequence having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence depicted in FIG. 7U. example, in some cases, a suitable RPGR polypeptide comprises an amino acid sequence having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence depicted in FIG. 7V.

Suitable polypeptides also include: CHM (choroideremia (Rab escort protein 1 (REP1))), a polypeptide that, when defective or missing, causes choroideremia (see, e.g., Donnelly et al. (1994) *Hum. Mol. Genet.* 3:1017; and van Bokhoven et al. (1994) *Hum. Mol. Genet.* 3:1041); and Crumbs homolog 1 (CRB1), a polypeptide that, when defective or missing, causes Leber congenital amaurosis and retinitis pigmentosa (see, e.g., den Hollander et al. (1999) *Nat. Genet.* 23:217; and GenBank Accession No. CAM23328). For example, a suitable REP1 polypeptide can comprise an amino acid having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence set depicted in FIG. 7G.

Suitable polypeptides include Rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit alpha (PDE6 $\alpha$ ), Rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit beta isoform 1 (PDE6 $\beta$  isoform 1), Rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit beta isoform 2 (PDE6 $\beta$  isoform 2), Rod cGMP-specific 3',5'-cyclic phosphodiesterase subunit beta isoform 3 (PDE6 $\beta$  isoform 3). For example, a suitable PDE6 $\alpha$  polypeptide can comprise an

amino acid having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence set depicted in FIG. 7K. As another example, a suitable PDE6 $\beta$  isoform 1 polypeptide can comprise an amino acid having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence set depicted in FIG. 7L. As another example, a suitable PDE6 $\beta$  isoform 2 polypeptide can comprise an amino acid having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence set depicted in FIG. 7M. As another example, a suitable PDE6 $\beta$  isoform 3 polypeptide can comprise an amino acid having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence set depicted in FIG. 7N.

Suitable polypeptides also include polypeptides that, when defective or missing, lead to achromotopsia, where such polypeptides include, e.g., cone photoreceptor cGMP-gated channel subunit alpha (CNGA3) (see, e.g., GenBank Accession No. NP\_001289; and Booij et al. (2011) *Ophthalmology* 118:160-167); cone photoreceptor cGMP-gated cation channel beta-subunit (CNGB3) (see, e.g., Kohl et al. (2005) *Eur J Hum Genet.* 13(3):302); guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 2 (GNAT2) (ACHM4); and ACHM5; and polypeptides that, when defective or lacking, lead to various forms of color blindness (e.g., L-opsin, M-opsin, and S-opsin). See Mancuso et al. (2009) *Nature* 461(7265):784-787.

For example, a suitable CNGA3 (also known as ACHM2) isoform 1 polypeptide can comprise an amino acid having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence set depicted in FIG. 7O. As another example, a suitable CNGA3 (also known as ACHM2) isoform 2 polypeptide can comprise an amino acid having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence set depicted in FIG. 7P.

As another example, a suitable CNGB3 (also known as ACHM3) polypeptide can comprise an amino acid having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence set depicted in FIG. 7Q. As another example, GNAT2 (also known as ACHM4) can comprise an amino acid having at least about 90%, at least about 95%, at least about 98%, at least about 99%, or 100%, amino acid sequence identity to the amino acid sequence set depicted in FIG. 7R.

#### Site-Specific Endonucleases

In some cases, a gene product of interest is a site-specific endonuclease that provide for site-specific knock-down of gene function, e.g., where the endonuclease knocks out an allele associated with a retinal disease. For example, where a dominant allele encodes a defective copy of a gene that, when wild-type, is a retinal structural protein and/or provides for normal retinal function, a site-specific endonuclease can be targeted to the defective allele and knock out the defective allele. In some cases, a site-specific endonuclease is an RNA-guided endonuclease.

In addition to knocking out a defective allele, a site-specific nuclease can also be used to stimulate homologous recombination with a donor DNA that encodes a functional copy of the protein encoded by the defective allele. Thus, e.g., a subject rAAV virion can be used to deliver both a site-specific endonuclease that knocks out a defective allele,

and can be used to deliver a functional copy of the defective allele, resulting in repair of the defective allele, thereby providing for production of a functional retinal protein (e.g., functional retinoschisin, functional RPE65, functional peripherin, etc.). See, e.g., Li et al. (2011) *Nature* 475:217. In some embodiments, a subject rAAV virion comprises a heterologous nucleotide sequence that encodes a site-specific endonuclease; and a heterologous nucleotide sequence that encodes a functional copy of a defective allele, where the functional copy encodes a functional retinal protein. Functional retinal proteins include, e.g., retinoschisin, RPE65, retinitis pigmentosa GTPase regulator (RGPR)-interacting protein-1, peripherin, peripherin-2, RdCVF, and the like.

Site-specific endonucleases that are suitable for use include, e.g., zinc finger nucleases (ZFNs); meganucleases; and transcription activator-like effector nucleases (TALENs), where such site-specific endonucleases are non-naturally occurring and are modified to target a specific gene. Such site-specific nucleases can be engineered to cut specific locations within a genome, and non-homologous end joining can then repair the break while inserting or deleting several nucleotides. Such site-specific endonucleases (also referred to as “INDELS”) then throw the protein out of frame and effectively knock out the gene. See, e.g., U.S. Patent Publication No. 2011/0301073. Suitable site-specific endonucleases include engineered meganuclease re-engineered homing endonucleases. Suitable endonucleases include an I-TevI nuclease. Suitable meganucleases include I-SceI (see, e.g., Bellaiche et al. (1999) *Genetics* 152:1037); and I-CreI (see, e.g., Heath et al. (1997) *Nature Structural Biology* 4:468).

#### RNA-Guided Endonucleases

In some cases, the gene product is an RNA-guided endonuclease. In some cases, the gene product is an RNA comprising a nucleotide sequence encoding an RNA-guided endonuclease. In some cases, the gene product is a guide RNA, e.g., a single-guide RNA. In some cases, the gene products are: 1) a guide RNA; and 2) an RNA-guided endonuclease. The guide RNA can comprise: a) a protein-binding region that binds to the RNA-guided endonuclease; and b) a region that binds to a target nucleic acid. An RNA-guided endonuclease is also referred to herein as a “genome editing nuclease.”

Examples of suitable genome editing nucleases are CRISPR/Cas endonucleases (e.g., class 2 CRISPR/Cas endonucleases such as a type II, type V, or type VI CRISPR/Cas endonucleases). Thus, a genome targeting composition can include a CRISPR/Cas endonuclease (e.g., a class 2 CRISPR/Cas endonuclease such as a type II, type V, or type VI CRISPR/Cas endonuclease). In some cases, a genome targeting composition includes a class 2 CRISPR/Cas endonuclease. In some cases, a genome targeting composition includes a class 2 type II CRISPR/Cas endonuclease (e.g., a Cas9 protein). In some cases, a genome targeting composition includes a class 2 type V CRISPR/Cas endonuclease (e.g., a Cpf1 protein, a C2c1 protein, or a C2c3 protein). In some cases, a genome targeting composition includes a class 2 type VI CRISPR/Cas endonuclease (e.g., a C2c2 protein).

In some cases, a genome editing nuclease is a fusion protein that is fused to a heterologous polypeptide (also referred to as a “fusion partner”). In some cases, a genome editing nuclease is fused to an amino acid sequence (a fusion partner) that provides for subcellular localization, i.e., the fusion partner is a subcellular localization sequence (e.g., one or more nuclear localization signals (NLSs) for targeting to the nucleus, two or more NLSs, three or more NLSs, etc.).

In some cases, the genome-editing endonuclease is a Type II CRISPR/Cas endonuclease. In some cases, the genome-editing endonuclease is a Cas9 polypeptide. The Cas9 protein is guided to a target site (e.g., stabilized at a target site) within a target nucleic acid sequence (e.g., a chromosomal sequence or an extrachromosomal sequence, e.g., an episomal sequence, a minicircle sequence, a mitochondrial sequence, a chloroplast sequence, etc.) by virtue of its association with the protein-binding segment of the Cas9 guide RNA. In some cases, a Cas9 polypeptide comprises an amino acid sequence having at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, at least 99%, or more than 99%, amino acid sequence identity to the *Streptococcus pyogenes* Cas9 depicted in FIG. 8A. In some cases, the Cas9 polypeptide used in a composition or method of the present disclosure is a *Staphylococcus aureus* Cas9 (saCas9) polypeptide. In some cases, the saCas9 polypeptide comprises an amino acid sequence having at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100%, amino acid sequence identity to the saCas9 amino acid sequence depicted in FIG. 8B.

In some cases, a suitable Cas9 polypeptide is a high-fidelity (HF) Cas9 polypeptide. Kleinstiver et al. (2016) *Nature* 529:490. For example, amino acids N497, R661, Q695, and Q926 of the amino acid sequence depicted in FIG. 8A are substituted, e.g., with alanine. For example, an HF Cas9 polypeptide can comprise an amino acid sequence having at least 90%, at least 95%, at least 98%, at least 99%, or 100%, amino acid sequence identity to the amino acid sequence depicted in FIG. 8A, where amino acids N497, R661, Q695, and Q926 are substituted, e.g., with alanine.

In some cases, a suitable Cas9 polypeptide exhibits altered PAM specificity. See, e.g., Kleinstiver et al. (2015) *Nature* 523:481.

In some cases, the genome-editing endonuclease is a type V CRISPR/Cas endonuclease. In some cases a type V CRISPR/Cas endonuclease is a Cpf1 protein. In some cases, a Cpf1 protein comprises an amino acid sequence having at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 90%, or 100%, amino acid sequence identity to the Cpf1 amino acid sequence depicted in FIG. 8C.

A nucleic acid that binds to a class 2 CRISPR/Cas endonuclease (e.g., a Cas9 protein; a type V or type VI CRISPR/Cas protein; a Cpf1 protein; etc.) and targets the complex to a specific location within a target nucleic acid is referred to herein as a “guide RNA” or “CRISPR/Cas guide nucleic acid” or “CRISPR/Cas guide RNA.” A guide RNA provides target specificity to the complex (the RNP complex) by including a targeting segment, which includes a guide sequence (also referred to herein as a targeting sequence), which is a nucleotide sequence that is complementary to a sequence of a target nucleic acid.

In some cases, a guide RNA includes two separate nucleic acid molecules: an “activator” and a “targeter” and is referred to herein as a “dual guide RNA”, a “double-molecule guide RNA”, a “two-molecule guide RNA”, or a “dgRNA.” In some cases, the guide RNA is one molecule (e.g., for some class 2 CRISPR/Cas proteins, the corresponding guide RNA is a single molecule; and in some cases, an activator and targeter are covalently linked to one another, e.g., via intervening nucleotides), and the guide RNA is referred to as a “single guide RNA”, a “single-molecule guide RNA”, a “one-molecule guide RNA”, or simply “sgRNA.”

Where the gene product is an RNA-guided endonuclease, or is both an RNA-guided endonuclease and a guide RNA, the gene product can modify a target nucleic acid. In some cases, e.g., where a target nucleic acid comprises a deleterious mutation in a defective allele (e.g., a deleterious mutation in a retinal cell target nucleic acid), the RNA-guided endonuclease/guide RNA complex, together with a donor nucleic acid comprising a nucleotide sequence that corrects the deleterious mutation (e.g., a donor nucleic acid comprising a nucleotide sequence that encodes a functional copy of the protein encoded by the defective allele), can be used to correct the deleterious mutation, e.g., via homology-directed repair (HDR).

In some cases, the gene products are an RNA-guided endonuclease and 2 separate sgRNAs, where the 2 separate sgRNAs provide for deletion of a target nucleic acid via non-homologous end joining (NHEJ).

The present disclosure provides a method of modifying a target nucleic acid in a retinal cell in an individual, where the target nucleic acid comprises a deleterious mutation, the method comprising administering to the individual (e.g., by intraocular; intravitreal; etc. administration) an rAAV virion of the present disclosure, where the rAAV virion comprises a heterologous nucleic acid comprising: i) a nucleotide sequence encoding an RNA-guided endonuclease (e.g., a Cas9 endonuclease); ii) a nucleotide sequence encoding a sgRNA that comprises a nucleotide sequence that is complementary to the target nucleic acid; and iii) a nucleotide sequence encoding a donor DNA template that comprises a nucleotide sequence that corrects the deleterious mutation. Administration of the rAAV virion results in correction of the deleterious mutation in the target nucleic acid by HDR.

The present disclosure provides a method of modifying a target nucleic acid in a retinal cell in an individual, where the target nucleic acid comprises a deleterious mutation, the method comprising administering to the individual (e.g., by intraocular; intravitreal; etc. administration) an rAAV virion of the present disclosure, where the rAAV virion comprises a heterologous nucleic acid comprising: i) a nucleotide sequence encoding an RNA-guided endonuclease (e.g., a Cas9 endonuclease); ii) a nucleotide sequence encoding a first sgRNA that comprises a nucleotide sequence that is complementary to a first sequence in the target nucleic acid; and iii) a nucleotide sequence encoding a second sgRNA that comprises a nucleotide sequence that is complementary to a second sequence in the target nucleic acid. Administration of the rAAV virion results in excision of the deleterious mutation in the target nucleic acid by NHEJ.

#### Regulatory Sequences

In some cases, a nucleotide sequence encoding a gene product of interest is operably linked to a transcriptional control element. For example, in some cases, a nucleotide sequence encoding a gene product of interest is operably linked to a constitutive promoter. In other cases, a nucleotide sequence encoding a gene product of interest is operably linked to an inducible promoter. In some instances, a nucleotide sequence encoding a gene product of interest is operably linked to a tissue-specific or cell type-specific regulatory element. For example, in some instances, a nucleotide sequence encoding a gene product of interest is operably linked to a retinal cell-specific promoter. For example, in some instances, a nucleotide sequence encoding a gene product of interest is operably linked to a photoreceptor-specific regulatory element (e.g., a photoreceptor-specific promoter), e.g., a regulatory element that confers selective expression of the operably linked gene in a photoreceptor cell. Suitable photoreceptor-specific regulatory elements

include, e.g., a rhodopsin promoter; a rhodopsin kinase promoter (Young et al. (2003) *Ophthalmol. Vis. Sci.* 44:4076); a beta phosphodiesterase gene promoter (Nicoud et al. (2007) *J. Gene Med.* 9:1015); a retinitis pigmentosa gene promoter (Nicoud et al. (2007) supra); an interphotoreceptor retinoid-binding protein (IRBP) gene enhancer (Nicoud et al. (2007) supra); an IRBP gene promoter (Yokoyama et al. (1992) *Exp Eye Res.* 55:225).

#### Pharmaceutical Compositions

The present disclosure provides a pharmaceutical composition comprising: a) a subject rAAV virion, as described above; and b) a pharmaceutically acceptable carrier, diluent, excipient, or buffer. In some embodiments, the pharmaceutically acceptable carrier, diluent, excipient, or buffer is suitable for use in a human.

Such excipients, carriers, diluents, and buffers include any pharmaceutical agent that can be administered without undue toxicity. Pharmaceutically acceptable excipients include, but are not limited to, liquids such as water, saline, glycerol and ethanol. Pharmaceutically acceptable salts can be included therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. A wide variety of pharmaceutically acceptable excipients are known in the art and need not be discussed in detail herein. Pharmaceutically acceptable excipients have been amply described in a variety of publications, including, for example, A. Gennaro (2000) "Remington: The Science and Practice of Pharmacy," 20th edition, Lippincott, Williams, & Wilkins; Pharmaceutical Dosage Forms and Drug Delivery Systems (1999) H. C. Ansel et al., eds., 7<sup>th</sup> ed., Lippincott, Williams, & Wilkins; and Handbook of Pharmaceutical Excipients (2000) A. H. Kibbe et al., eds., 3<sup>rd</sup> ed. Amer. Pharmaceutical Assoc. Methods of Delivering a Gene Product to a Retinal Cell and Treatment Methods

The present disclosure provides a method of delivering a gene product to a retinal cell in an individual, the method comprising administering to the individual a subject rAAV virion as described above. The gene product can be a polypeptide or an interfering RNA (e.g., an shRNA, an siRNA, and the like), an aptamer, or a site-specific endonuclease (e.g., an RNA-guided endonuclease), as described above. Delivering a gene product to a retinal cell can provide for treatment of a retinal disease. The retinal cell can be a photoreceptor, a retinal ganglion cell, a Müller cell, a bipolar cell, an amacrine cell, a horizontal cell, or a retinal pigmented epithelial cell. In some cases, the retinal cell is a photoreceptor cell, e.g., a rod or cone cell.

The present disclosure provides a method modifying a target nucleic acid in a retinal cell, the method comprising contacting the retinal cell with: 1) an rAAV virion of the present disclosure, wherein the rAAV virion comprises a heterologous nucleic acid comprising a nucleotide sequence encoding an RNA-guided endonuclease that binds a guide RNA; and 2) the guide RNA. The present disclosure provides a method modifying a target nucleic acid in a retinal cell, the method comprising contacting the retinal cell with an rAAV virion of the present disclosure, wherein the rAAV virion comprises a heterologous nucleic acid comprising a nucleotide sequence encoding: i) an RNA-guided endonuclease that binds a guide RNA; and ii) the guide RNA. In some cases, the method comprises contacting the retinal cell with a donor DNA template. In some cases, the RNA-guided



endonuclease is a Cas9 polypeptide. In some cases, the guide RNA is a single-guide RNA.

The present disclosure provides a method of treating an ocular disease (e.g., a retinal disease), the method comprising administering to an individual in need thereof an effective amount of a subject rAAV virion as described above. A subject rAAV virion can be administered via intraocular injection, by intravitreal injection, or by any other convenient mode or route of administration. Other convenient modes or routes of administration include, e.g., intravenous, intranasal, etc.

A “therapeutically effective amount” will fall in a relatively broad range that can be determined through experimentation and/or clinical trials. For example, for in vivo injection, i.e., injection directly into the eye, a therapeutically effective dose will be on the order of from about  $10^6$  to about  $10^{15}$  of the rAAV virions, e.g., from about  $10^8$  to  $10^{12}$  rAAV virions. For in vitro transduction, an effective amount of rAAV virions to be delivered to cells will be on the order of from about  $10^9$  to about  $10^{13}$  of the rAAV virions. Other effective dosages can be readily established by one of ordinary skill in the art through routine trials establishing dose response curves.

In some embodiments, more than one administration (e.g., two, three, four or more administrations) may be employed to achieve the desired level of gene expression. In some cases, the more than one administration is administered at various intervals, e.g., daily, weekly, twice monthly, monthly, every 3 months, every 6 months, yearly, etc. In some cases, multiple administrations are administered over a period of time of from 1 month to 2 months, from 2 months to 4 months, from 4 months to 8 months, from 8 months to 12 months, from 1 year to 2 years, from 2 years to 5 years, or more than 5 years.

Ocular diseases that can be treated using a subject method include, but are not limited to, acute macular neuroretinopathy; Behcet’s disease; choroidal neovascularization; diabetic uveitis; histoplasmosis; macular degeneration, such as acute macular degeneration, non-exudative age related macular degeneration and exudative age related macular degeneration; edema, such as macular edema, cystoid macular edema and diabetic macular edema; multifocal choroiditis; ocular trauma which affects a posterior ocular site or location; ocular tumors; retinal disorders, such as central retinal vein occlusion, diabetic retinopathy (including proliferative diabetic retinopathy), proliferative vitreoretinopathy (PVR), retinal arterial occlusive disease, retinal detachment, uveitic retinal disease; sympathetic ophthalmia; Vogt Koyanagi-Harada (VKH) syndrome; uveal diffusion; a posterior ocular condition caused by or influenced by an ocular laser treatment; posterior ocular conditions caused by or influenced by a photodynamic therapy; photocoagulation, radiation retinopathy; epiretinal membrane disorders; branch retinal vein occlusion; anterior ischemic optic neuropathy; non-retinopathy diabetic retinal dysfunction; retinoschisis; retinitis pigmentosa; glaucoma; Usher syndrome, cone-rod dystrophy; Stargardt disease (fundus flavimaculatus); inherited macular degeneration; chorioretinal degeneration; Leber congenital amaurosis; congenital stationary night blindness; choroideremia; Bardet-Biedl syndrome; macular telangiectasia; Leber’s hereditary optic neuropathy; retinopathy of prematurity; disorders of color vision, including achromatopsia, protanopia, deuteranopia, and tritanopia; and Bietti’s crystalline dystrophy.

#### Nucleic Acids and Host Cells

The present disclosure provides an isolated nucleic acid comprising a nucleotide sequence that encodes a subject

variant adeno-associated virus (AAV) capsid protein as described above, where the variant AAV capsid protein comprises an insertion of from about 5 amino acids to about 20 amino acids in the GH loop or loop IV relative to a corresponding parental AAV capsid protein, and where the variant capsid protein, when present in an AAV virion, provides for increased infectivity of a retinal cell compared to the infectivity of the retinal cell by an AAV virion comprising the corresponding parental AAV capsid protein. A subject isolated nucleic acid can be an AAV vector, e.g., a recombinant AAV vector.

#### Insertion Peptides

A variant AAV capsid protein encoded by a subject nucleic acid has an insertion peptide of from about 5 amino acids to about 20 amino acids in length is inserted into the GH loop of an AAV capsid. The insertion peptide has a length of 5 amino acids, 6 amino acids, 7 amino acids, 8 amino acids, 9 amino acids, 10 amino acids, 11 amino acids, 12 amino acids, 13 amino acids, 14 amino acids, 15 amino acids, 16 amino acids, 17 amino acids, 18 amino acids, 19 amino acids, or 20 amino acids. Suitable insertion peptides are as described above. Suitable insertion peptides include a peptide of any one of Formulas I-X, as described above.

A subject recombinant AAV vector can be used to generate a subject recombinant AAV virion, as described above. Thus, the present disclosure provides a recombinant AAV vector that, when introduced into a suitable cell, can provide for production of a subject recombinant AAV virion.

The present invention further provides host cells, e.g., isolated (genetically modified) host cells, comprising a subject nucleic acid. A subject host cell can be an isolated cell, e.g., a cell in in vitro culture. A subject host cell is useful for producing a subject rAAV virion, as described below. Where a subject host cell is used to produce a subject rAAV virion, it is referred to as a “packaging cell.” In some embodiments, a subject host cell is stably genetically modified with a subject nucleic acid. In other embodiments, a subject host cell is transiently genetically modified with a subject nucleic acid.

A subject nucleic acid is introduced stably or transiently into a host cell, using established techniques, including, but not limited to, electroporation, calcium phosphate precipitation, liposome-mediated transfection, and the like. For stable transformation, a subject nucleic acid will generally further include a selectable marker, e.g., any of several well-known selectable markers such as neomycin resistance, and the like.

A subject host cell is generated by introducing a subject nucleic acid into any of a variety of cells, e.g., mammalian cells, including, e.g., murine cells, and primate cells (e.g., human cells). Suitable mammalian cells include, but are not limited to, primary cells and cell lines, where suitable cell lines include, but are not limited to, 293 cells, COS cells, HeLa cells, Vero cells, 3T3 mouse fibroblasts, C3H10T1/2 fibroblasts, CHO cells, and the like. Non-limiting examples of suitable host cells include, e.g., HeLa cells (e.g., American Type Culture Collection (ATCC) No. CCL-2), CHO cells (e.g., ATCC Nos. CRL9618, CCL61, CRL9096), 293 cells (e.g., ATCC No. CRL-1573), Vero cells, NIH 3T3 cells (e.g., ATCC No. CRL-1658), Huh-7 cells, BHK cells (e.g., ATCC No. CCL10), PC12 cells (ATCC No. CRL1721), COS cells, COS-7 cells (ATCC No. CRL1651), RAT1 cells, mouse L cells (ATCC No. CCLI.3), human embryonic kidney (HEK) cells (ATCC No. CRL1573), HLHepG2 cells, and the like. A subject host cell can also be made using a baculovirus to infect insect cells such as Sf9 cells, which

produce AAV (see, e.g., U.S. Pat. No. 7,271,002; U.S. patent application Ser. No. 12/297,958)

In some embodiments, a subject genetically modified host cell includes, in addition to a nucleic acid comprising a nucleotide sequence encoding a variant AAV capsid protein, as described above, a nucleic acid that comprises a nucleotide sequence encoding one or more AAV rep proteins. In other embodiments, a subject host cell further comprises an rAAV vector. An rAAV virion can be generated using a subject host cell. Methods of generating an rAAV virion are described in, e.g., U.S. Patent Publication No. 2005053922 and U.S. Patent Publication No. 2009/0202490.

#### Examples of Non-Limiting Aspects of the Disclosure

Aspects, including embodiments, of the present subject matter described above may be beneficial alone or in combination, with one or more other aspects or embodiments. Without limiting the foregoing description, certain non-limiting aspects of the disclosure numbered 1-34 are provided below. As will be apparent to those of skill in the art upon reading this disclosure, each of the individually numbered aspects may be used or combined with any of the preceding or following individually numbered aspects. This is intended to provide support for all such combinations of aspects and is not limited to combinations of aspects explicitly provided below:

Aspect 1. A recombinant adeno-associated virus (rAAV) virion comprising: a) a variant AAV capsid protein, wherein the variant AAV capsid protein comprises an insertion of a heterologous peptide having a length of from about 5 amino acids to about 20 amino acids in the capsid protein GH loop relative to a corresponding parental AAV capsid protein, and wherein the variant capsid protein confers increased infectivity of a retinal cell compared to the infectivity of the retinal cell by a control AAV virion comprising the corresponding parental AAV capsid protein; and b) a heterologous nucleic acid comprising a nucleotide sequence encoding a heterologous gene product.

Aspect 2. The rAAV virion of aspect 1, wherein the rAAV virion exhibits at least 5-fold increased infectivity of a retinal cell compared to the infectivity of the retinal cell by a control AAV virion comprising the corresponding parental AAV capsid protein.

Aspect 3. The rAAV virion of aspect 1, wherein the rAAV virion exhibits at least 10-fold increased infectivity of a retinal cell compared to the infectivity of the retinal cell by an AAV virion comprising the corresponding parental AAV capsid protein.

Aspect 4. The rAAV virion of any one of aspects 1-3, wherein the rAAV virion exhibits at least 5-fold increased localization to one or more of the inner nuclear layer, the outer nuclear layer, the photoreceptor layer, the ganglion cell layer, and the retinal pigment epithelium, compared to the extent of localization to the inner nuclear layer, the outer nuclear layer, the photoreceptor layer, the ganglion cell layer, or the retinal pigment epithelium, by an AAV virion comprising the corresponding parental AAV capsid protein.

Aspect 5. The rAAV virion of any one of aspects 1-4, wherein the insertion site is between amino acids corresponding to amino acids 570 and 611 of VP1 of AAV2, or the corresponding position in the capsid protein of another AAV serotype.

Aspect 6. The rAAV virion of any one of aspects 1-5, wherein the insertion site is located between amino acids corresponding to amino acids 587 and 588 of VP1 of AAV2, or the corresponding position in the capsid protein of another AAV serotype.

Aspect 7. The rAAV virion of any one of aspects 1-6, wherein gene product is an interfering RNA or an aptamer.

Aspect 8. The rAAV virion of any one of aspects 1-6, wherein the gene product is a polypeptide.

Aspect 9. The rAAV virion of aspect 8, wherein the polypeptide is a neuroprotective polypeptide, an anti-angiogenic polypeptide, or a polypeptide that enhances function of a retinal cell.

Aspect 10. The rAAV virion of aspect 8, wherein the polypeptide is an RNA-guided endonuclease.

Aspect 11. The rAAV virion of aspect 10, wherein the RNA-guided endonuclease is a Cas9 polypeptide.

Aspect 12. The rAAV virion of aspect 10, wherein the gene product is an RNA-guided endonuclease and a guide RNA.

Aspect 13. The rAAV virion of any one of aspects 1-12, wherein the heterologous peptide inserted into the GH loop is of any one of Formulas I-X.

Aspect 14. The rAAV virion of any one of aspects 1-12, wherein the heterologous peptide is a peptide of Formula I:  $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ ,

wherein:

$X_1$  is Leu, Ile, Pro, or Gln;

$X_2$  is Ala, Pro, Ser, Asp, Gly, Thr, or Val;

$X_3$  is Lys, His, Thr, Ile, Pro, Val, Arg, Ala, Asp, Glu, Asn, Gln, or Tyr;

$X_4$ , if present, is Gln, Asp, Ser, Gly, Thr, Ile, Asn, Glu, Lys, or Arg;

$X_5$  is Asp, Ser, Gln, Val, Thr, Gly, Ala, Asn, Lys, or Tyr;

$X_6$  is Thr, Ala, Gln, Ser, Glu, Pro, or Ile;

$X_7$  is Thr, Ser, Asn, Pro, Leu, Gln, Lys, Ala, or Cys;

$X_8$  is Lys, Ser, Arg, Thr, Ala, Glu, Ile, or Asn;

$X_9$  is Asn, Pro, Ser, Lys, His, Ile, Thr, or Ala; and

$X_{10}$  is Ala, Phe, Asp, Thr, Val, or Met.

Aspect 15. The rAAV virion of aspect 14, wherein the heterologous peptide comprises one of the following amino acid sequences: (1) LAKDATKNA (SEQ ID NO:47); (2) PAHQDTTKNA (SEQ ID NO:48); (3) LAHQDTTKNA (SEQ ID NO:49); (4) LATTSQNKPA (SEQ ID NO:50); (5) LAISDQTKHA (SEQ ID NO:51); (6) IARGVAPSSA (SEQ ID NO:52); (7) LAPDSTRSA (SEQ ID NO:53); (8) LAKGTELKPA (SEQ ID NO:54); (9) LAIIDATKNA (SEQ ID NO:55); (10) LAVDGAQRSA (SEQ ID NO:56); (11) PAPQDTTKKA (SEQ ID NO:57); (12) LPHQDTTKNA (SEQ ID NO:58); (13) LAKDATKTIA (SEQ ID NO:59); (14) LAKQQSASTA (SEQ ID NO:60); (15) LAKSDQSKPA (SEQ ID NO:61); (16) LSHQDTTKNA (SEQ ID NO:62); (17) LAANQPSKPA (SEQ ID NO:63); (18) LAVSDSTKAA (SEQ ID NO:64); (19) LAAQGTAKKPA (SEQ ID NO:65); (20) LAPDQTTRNA (SEQ ID NO:66); (21) LAASDSTKAA (SEQ ID NO:67); (22) LAPQDTTKNA (SEQ ID NO:68); (23) LAKADETRPA (SEQ ID NO:69); (24) LAHQDTTKNA (SEQ ID NO:70); (25) LAHQDTTKNA (SEQ ID NO:71); (26) LAHQDTTKHA (SEQ ID NO:72); (27) LAHQDTTKKA (SEQ ID NO:73); (28) LAHQDTTRNA (SEQ ID NO:74); (29) LAHQDTTNA (SEQ ID NO:75); (30) LAHQGTTKNA (SEQ ID NO:76); (31) LAHQVTTKNA (SEQ ID NO:77); (32) LAISDQSKPA (SEQ ID NO:78); (33) LADATKTA (SEQ ID NO:79); (34) LAKDITTKNA (SEQ ID NO:80); (35) LAKSDQSRPA (SEQ ID NO:81); (36) LAPQDTTKNA (SEQ ID NO:82); (37) LATSDSTKAA (SEQ ID NO:83); (38) LAVDGSQRSA (SEQ ID NO:84); (39) LPISDQTKHA (SEQ ID NO:85); (40) LPKDATKTIA (SEQ ID NO:86); (41) LPPQDTTKNA (SEQ ID NO:87); (42) PAPQDTTKNA (SEQ ID NO:88); (43) QAHQDTTKNA (SEQ ID NO:89); (44) LAHETSPRPA (SEQ ID

NO:90); (45) LAKSTSTAPA (SEQ ID NO:91); (46) LADQDTTKNA (SEQ ID NO:92); (47) LAESDQSKPA (SEQ ID NO:93); (48) LAHKDTTKNA (SEQ ID NO:94); (49) LAHKTQQKM (SEQ ID NO:95); (50) LAHQDTTENA (SEQ ID NO:96); (51) LAHQDTTINA (SEQ ID NO:97); (52) LAHQDTTKKT (SEQ ID NO:98); (53) LAHQDTTKND (SEQ ID NO:99); (54) LAHQDTTKNT (SEQ ID NO:100); (55) LAHQDTTKNV (SEQ ID NO:101); (56) LAHQDTTKTM (SEQ ID NO:102); (57) LAHQNTTKNA (SEQ ID NO:103); (58) LAHRDTTKNA (SEQ ID NO:104); (59) LAISDQTNHA (SEQ ID NO:105); (60) LAKQKSASTA (SEQ ID NO:106); (61) LAKSDQCKPA (SEQ ID NO:107); (62) LAKSDQSKPD (SEQ ID NO:108); (63) LAKSDQSNPA (SEQ ID NO:109); (64) LAKSYQSKPA (SEQ ID NO:110); (65) LANQDTTKNA (SEQ ID NO:111); (66) LAPQNTTKNA (SEQ ID NO:112); (67) LAPSSIQKPA (SEQ ID NO:113); (68) LAQQDTTKNA (SEQ ID NO:114); (69) LAYQDTTKNA (SEQ ID NO:115); (70) LDHQDTTKNA (SEQ ID NO:116); (71) LDHQDTTKSA (SEQ ID NO:117); (72) LGHQDTTKNA (SEQ ID NO:118); (73) LPHQDTTKND (SEQ ID NO:119); (74) LPHQDTTKNT (SEQ ID NO:120); (75) LPHQDTTNNA (SEQ ID NO:121); (76) LTHQDTTKNA (SEQ ID NO:122); (77) LTKDATKTIA (SEQ ID NO:123); (78) LTPQDTTKNA (SEQ ID NO:124); and (79) LVHQDTTKNA (SEQ ID NO:125).

Aspect 16. The rAAV virion of any one of aspects 1-12, wherein the heterologous peptide is a peptide of Formula II:

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ , wherein:

$X_1$  is Leu, Ile, or Pro;

$X_2$  is Ala, Pro, or Ser;

$X_3$  is Lys, His, Thr, Ile, Pro, Val, Arg, or Ala;

$X_4$  (if present) is Gln, Asp, Ser, Gly, Thr, Ile, or Asn;

$X_5$  is Asp, Ser, Gln, Val, Thr, Gly, or Ala;

$X_6$  is Thr, Ala, Gln, Ser, Glu, or Pro;

$X_7$  is Thr, Ser, Asn, Pro, Leu, Gln, Lys, or Ala;

$X_8$  is Lys, Ser, Arg, or Thr;

$X_9$  is Asn, Pro, Ser, Lys, His, Ile, Thr, or Ala; and

$X_{10}$  is Ala.

Aspect 17. The rAAV virion of aspect 16, wherein the peptide comprises one of the following amino acid sequences: (1) LAKDATKNA (SEQ ID NO:47); (2) PAHQDTTKNA (SEQ ID NO:48); (3) LAHQDTTKNA (SEQ ID NO:49); (4) LATTSQNKPA (SEQ ID NO:50); (5) LAISDQTKHA (SEQ ID NO:51); (6) IARGVAPSSA (SEQ ID NO:52); (7) LAPDSTTRSA (SEQ ID NO:53); (8) LAKGTELKPA (SEQ ID NO:54); (9) LAIIDATKNA (SEQ ID NO:55); (10) LAVDGAQRSA (SEQ ID NO:56); (11) PAPQDTTKKA (SEQ ID NO:57); (12) LPHQDTTKNA (SEQ ID NO:58); (13) LAKDATKTIA (SEQ ID NO:59); (14) LAKQQSASTA (SEQ ID NO:60); (15) LAKSDQSKPA (SEQ ID NO:61); (16) LSHQDTTKNA (SEQ ID NO:62); (17) LAANQPSKPA (SEQ ID NO:63); (18) LAVSDSTKAA (SEQ ID NO:64); (19) LAAQGTAKKPA (SEQ ID NO:65); (20) LAPDQTTRNA (SEQ ID NO:66); (21) LAASDSTKAA (SEQ ID NO:67); (22) LAPQDTTKNA (SEQ ID NO:68); (23) LAKADETRPA (SEQ ID NO:69); (24) LAHQDTAKNA (SEQ ID NO:70); (25) LAHQDTTKNA (SEQ ID NO:71); (26) LAHQDTTKHA (SEQ ID NO:72); (27) LAHQDTTKKA (SEQ ID NO:73); (28) LAHQDTRRNA (SEQ ID NO:74); (29) LAHQDTTNA (SEQ ID NO:75); (30) LAHQGTTKNA (SEQ ID NO:76); (31) LAHQVTTKNA (SEQ ID NO:77); (32) LAISDQSKPA (SEQ ID NO:78); (33) LADATKTA (SEQ ID NO:79); (34) LAKDTTKNA (SEQ ID NO:80); (35) LAKSDQSRPA (SEQ ID NO:81); (36)

LAPQDTTKNA (SEQ ID NO:82); (37) LATSDSTKAA (SEQ ID NO:83); (38) LAVDGSQRSA (SEQ ID NO:84); (39) LPISDQTKHA (SEQ ID NO:85); (40) LPKDATKTIA (SEQ ID NO:86); (41) LPPQDTTKNA (SEQ ID NO:87); and (42) PAPQDTTKNA (SEQ ID NO:88).

Aspect 18. The rAAV virion of aspect 16, wherein the peptide comprises one of the following amino acid sequences: (1) LAKDATKNA (SEQ ID NO:47); (2) PAHQDTTKNA (SEQ ID NO:48); (3) LAHQDTTKNA (SEQ ID NO:49); (4) LATTSQNKPA (SEQ ID NO:50); (5) LAISDQTKHA (SEQ ID NO:51); (6) IARGVAPSSA (SEQ ID NO:52); (7) LAPDSTTRSA (SEQ ID NO:53); (8) LAKGTELKPA (SEQ ID NO:54); (9) LAIIDATKNA (SEQ ID NO:55); (10) LAVDGAQRSA (SEQ ID NO:56); (11) PAPQDTTKKA (SEQ ID NO:57); (12) LPHQDTTKNA (SEQ ID NO:58); (13) LAKDATKTIA (SEQ ID NO:59); (14) LAKQQSASTA (SEQ ID NO:60); (15) LAKSDQSKPA (SEQ ID NO:61); (16) LSHQDTTKNA (SEQ ID NO:62); (17) LAANQPSKPA (SEQ ID NO:63); and (18) LAVSDSTKAA (SEQ ID NO:64).

Aspect 19. A pharmaceutical composition comprising: a) a recombinant adeno-associated virus virion of any one of aspects 1-18; and b) a pharmaceutically acceptable excipient.

Aspect 20. A method of delivering a gene product to a retinal cell in an individual, the method comprising administering to the individual a recombinant adeno-associated virus (rAAV) virion according any one of aspects 1-18.

Aspect 21. The method of aspect 20, wherein the gene product is a polypeptide.

Aspect 22. The method of aspect 20, wherein the gene product is a short interfering RNA or an aptamer.

Aspect 23. The method of aspect 21, wherein the polypeptide is a neuroprotective factor, an anti-angiogenic polypeptide, an anti-apoptotic factor, or a polypeptide that enhances function of a retinal cell.

Aspect 24. The method of aspect 21, wherein the polypeptide is glial derived neurotrophic factor, fibroblast growth factor 2, neurturin, ciliary neurotrophic factor, nerve growth factor, brain derived neurotrophic factor, epidermal growth factor, rhodopsin, X-linked inhibitor of apoptosis, retinoschisin, RPE65, retinitis pigmentosa GTPase-interacting protein-1, peripherin, peripherin-2, a rhodopsin, RdCVF, retinitis pigmentosa GTPase regulator (RPGR), or Sonic hedgehog.

Aspect 25. The method of aspect 21, wherein the polypeptide is an RNA-guided endonuclease.

Aspect 26. A method of treating an ocular disease, the method comprising administering to an individual in need thereof an effective amount of a recombinant adeno-associated virus (rAAV) virion according to any one of aspects 1-18.

Aspect 27. The method of aspect 26, wherein said administering is by intraocular injection.

Aspect 28. The method of aspect 26, wherein said administering is by intravitreal injection.

Aspect 29. The method of aspect 26, wherein the ocular disease is glaucoma, retinitis pigmentosa, macular degeneration, retinoschisis, Leber's Congenital Amaurosis, diabetic retinopathy, achromotopsia, or color blindness.

Aspect 30. An isolated nucleic acid comprising a nucleotide sequence that encodes a variant adeno-associated virus (AAV) capsid protein, wherein the variant AAV capsid protein comprises an insertion of from about 5 amino acids to about 20 amino acids in the capsid protein GH loop relative to a corresponding parental AAV capsid protein, and wherein the variant capsid protein, when present in an AAV

virion, provides for increased infectivity of the AAV virion of a retinal cell, and wherein the amino acid insertion is in the GH loop of a native AAV capsid, wherein the insertion is a peptide of any one of Formulas I-X.

Aspect 31. The isolated nucleic acid of aspect 30, wherein the insertion site is between amino acids 587 and 588 of AAV2, between amino acids 590 and 591 of AAV1, between amino acids 575 and 576 of AAV5, between amino acids 590 and 591 of AAV6, between amino acids 589 and 590 of AAV7, between amino acids 590 and 591 of AAV8, between amino acids 588 and 589 of AAV9, or between amino acids 588 and 589 of AAV10.

Aspect 32. An isolated, genetically modified host cell comprising the nucleic acid of aspect 30 or aspect 31.

Aspect 33. A variant adeno-associated virus (AAV) capsid protein, wherein the variant AAV capsid protein comprises an insertion of from about 5 amino acids to about 20 amino acids wherein the amino acid insertion is in the GH loop of a native AAV capsid, wherein the insertion is a peptide of any one of Formulas I-X.

Aspect 34. In any of aspects 1-33, the heterologous peptide that is inserted into the GH loop can be of one of Formulas I-X, where:

Formula I is  $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ , where:

$X_1$  is Leu, Ile, Pro, or Gln;

$X_2$  is Ala, Pro, Ser, Asp, Gly, Thr, or Val;

$X_3$  is Lys, His, Thr, Ile, Pro, Val, Arg, Ala, Asp, Glu, Asn, Gln, or Tyr;

$X_4$  (if present) is Gln, Asp, Ser, Gly, Thr, Ile, Asn, Glu, Lys, or Arg;

$X_5$  is Asp, Ser, Gln, Val, Thr, Gly, Ala, Asn, Lys, or Tyr;

$X_6$  is Thr, Ala, Gln, Ser, Glu, Pro, or Ile;

$X_7$  is Thr, Ser, Asn, Pro, Leu, Gln, Lys, Ala, or Cys;

$X_8$  is Lys, Ser, Arg, Thr, Ala, Glu, Ile, or Asn;

$X_9$  is Asn, Pro, Ser, Lys, His, Ile, Thr, or Ala; and

$X_{10}$  is Ala, Phe, Asp, Thr, Val, or Met;

Formula II is  $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ , where:

$X_1$  is Leu, Ile, or Pro;

$X_2$  is Ala, Pro, or Ser;

$X_3$  is Lys, His, Thr, Ile, Pro, Val, Arg, or Ala;

$X_4$  (if present) is Gln, Asp, Ser, Gly, Thr, Ile, or Asn;

$X_5$  is Asp, Ser, Gln, Val, Thr, Gly, or Ala;

$X_6$  is Thr, Ala, Gln, Ser, Glu, or Pro;

$X_7$  is Thr, Ser, Asn, Pro, Leu, Gln, Lys, or Ala;

$X_8$  is Lys, Ser, Arg, or Thr;

$X_9$  is Asn, Pro, Ser, Lys, His, Ile, Thr, or Ala; and

$X_{10}$  is Ala;

Formula III is  $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ , where:

$X_1$  is Leu, Ile, or Pro;

$X_2$  is Ala, Pro, or Ser;

$X_3$  is Lys, His, Thr, Ile, Pro, Val, Arg, or Ala;

$X_4$  (if present) is Gln, Asp, Ser, Gly, Thr, Ile, or Asn;

$X_5$  is Asp, Ser, Gln, Val, Thr, Gly, or Ala;

$X_6$  is Thr, Ala, Gln, Ser, Glu, or Pro;

$X_7$  is Thr, Ser, Asn, Pro, Leu, Gln, Lys, or Ala;

$X_8$  is Lys, Ser, Arg, or Thr;

$X_9$  is Asn, Pro, Ser, Lys, His, Ile, Thr, or Ala; and

$X_{10}$  is Ala, Thr, Asp Val, or Met;

Formula IV is  $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ , where:

$X_1$  is Leu;

$X_2$  is Ala;

$X_3$  is Lys, His, Thr, Ile, Pro, or Val;

$X_4$  (if present) is Gln, Asp, Ser, or Gly;

$X_5$  is Asp, Ser, or Gln;

$X_6$  is Thr, Ala, Gln, or Ser;

$X_7$  is Thr or Ser;

$X_8$  is Lys, Ser, or Arg;

$X_9$  is Asn, Pro, or Ser; and

$X_{10}$  is Ala;

Formula V is  $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ , where:

$X_1$  is Leu;

$X_2$  is Ala;

$X_3$  is Lys or His;

$X_4$  (if present) is Gln, Asp, Ser, or Gly;

$X_5$  is Asp, Ser, or Gln;

$X_6$  is Thr, Ala, Gln, or Ser;

$X_7$  is Thr or Ser;

$X_8$  is Lys, Ser, or Arg;

$X_9$  is Asn, Pro, or Ser; and

$X_{10}$  is Ala;

Formula VI is  $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ , where:

$X_1$  is Leu;

$X_2$  is Ala;

$X_3$  is Asn, Lys, Thr, Gln, Ser, Ile, or Leu;

$X_4$  is Ser, Ala, Thr, Glu, Gln, Gly, Lys, or Pro;

$X_5$  is Asp, Pro, Glu, Thr, Asn, or Arg;

$X_6$  is Ile, His, Thr, Gln, Asn, Tyr, Asp, or Glu;

$X_7$  is Gln, Thr, Asn, Ala, or Lys;

$X_8$  is Lys, Thr, Arg, or Asp;

$X_9$  is Pro, Asn, Thr, Arg, Lys, or Ser; and

$X_{10}$  is Ala;

Formula VII is LAHQDTTKX<sub>1</sub>X<sub>2</sub>X<sub>3</sub>(SEQ ID NO:148), where  $X_1$  is Lys, Thr, Asn, or His;  $X_2$  is Ala, Thr, Val, Ile, Met, or Asp; and  $X_3$ , if present, is Ala;

Formula VIII is LAX<sub>1</sub>QX<sub>2</sub>TX<sub>3</sub>X<sub>4</sub>X<sub>5</sub>X<sub>6</sub> (SEQ ID NO:149), where  $X_1$  is Ala, Pro, Asp, or His;  $X_2$  is Gly or Asp;  $X_3$  is Ala, Thr, or Lys;  $X_4$  is Asn, Glu, Lys, Arg, or Thr;  $X_5$  is Leu, Asn, Lys, or Thr; and  $X_6$ , if present, is Ala, Thr, Asp, Val, or Met;

Formula IX is X<sub>1</sub>AX<sub>2</sub>X<sub>3</sub>DX<sub>4</sub>TKX<sub>5</sub>A (SEQ ID NO:150), where  $X_1$  is Val or Leu;  $X_2$  is Ile, Val, His, or Asp;  $X_3$  is Glu, Ser, Lys, or Gln;  $X_4$  is His, Ser, or Thr; and  $X_5$  is Ser, Ala, Asn, His, or Lys; and

Formula X is X<sub>1</sub>X<sub>2</sub>X<sub>3</sub>AX<sub>4</sub>QX<sub>5</sub>TX<sub>6</sub>KNA (SEQ ID NO:151), where  $X_1$ , if present, is Leu;  $X_2$ , if present, is Ala;  $X_3$  is Lys, Leu, or Pro;  $X_4$  is Asn, His, Pro, or Tyr;  $X_5$  is Asn, Gly, Val, or Asp; and  $X_6$  is Pro or Thr.

## EXAMPLES

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the present invention, and are not intended to limit the scope of what the inventors regard as their invention nor are they intended to represent that the experiments below are all or the only experiments performed. Efforts have been made to ensure accuracy with respect to numbers used (e.g. amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is weight average molecular weight, temperature is in degrees Celsius, and pressure is at or near atmospheric. Standard abbreviations may be used, e.g., bp, base pair(s); kb, kilobase(s); pl, picoliter(s); s or sec, second(s); min, minute(s); h or hr, hour(s); aa, amino acid(s); kb, kilobase(s); bp, base pair(s); nt, nucleotide(s); i.m., intramuscular(ly); i.p., intraperitoneal(ly); s.c., subcutaneous(ly); and the like.

### Example 1: Generation and Characterization of AAV Virions with AAV Capsid Variants

An iterative in vivo screening methodology was used to create AAV with capsid variants able to overcome the

significant and complex barriers preventing panretinal AAV infection in a large animal eye. Dogs are an important preclinical model for retinal degenerative disease, with an eye size and structure similar to humans, and many forms of retinal disease are naturally occurring in a variety of dog breeds. The screening method was used to identify 96 AAV variants capable of panretinal infection in the canine retina. Deep sequencing was used to quantify the performance of 18 of these variants from the pool of screened AAV variants in canine retina. Infectivity was quantified based on levels of viral DNA and mRNA in retinal cells following intravitreal injection. These variants can be used for a wide variety of gene delivery strategies in large animal and human eyes.

A peptide display library containing a random 21-nucleotide insert (surrounded by a 5' 6-nucleotide linker and a 3' 3-nucleotide linker) at a surface exposed position on the AAV capsid was created. Virus was packaged such that each viral genome was encapsidated within the capsid protein shell that that genome encoded. Therefore functional improvements identified through selection can be linked to the genome sequence contained within the viral capsid. From this library, an iterative in vivo screening selection process was used to identify variants with the ability to infect the canine retina from the vitreous (FIG. 1). Canine eyes were injected in each round with ~250  $\mu$ L of 10E+13-10E+14 viral genomes/mL (vg/mL) titer virus. Three weeks after injection, eyes were enucleated, and retinal punches were taken from central and peripheral regions of the retina. RPE cells were separated from retinal tissue, and tissue was frozen. DNA was then collected from retinal cells, and cap genes were polymerase chain reaction (PCR) amplified from isolated samples. Cap genes were used for subsequent AAV packaging.

FIG. 1. Illustration of the directed evolution methodology used to develop canine retinal AAV variants. Peptide display libraries were created, packaged into AAV vectors, and injected into the canine eye via intravitreal injections. Iterative round of selection were used to positively select AAV variants from the pool of vectors. Three rounds of selection were followed by a round of error prone PCR, followed by additional selection rounds.

Following 5 rounds of selection, Illumina deep sequencing was used to identify variants that increased over the rounds in relative representation in the library of AAV variants. An increase of representation in the viral library indicates positive selection and ability to infect the canine retina from the vitreous. Out of a library of ~10E+7 variants, the top 96 variants that were selected for in the in vivo screen are provided in Table 1.

TABLE 1

	Peptide No.	SEQID NO:	
	LAKDATKNA	1	47
	PAHQDTTKNA	2	48
	LAHQDTTKNA	3	49
	LATTSQNKPA	4	50
	LAISDQTKHA	5	51
	IARGVAPSSA	6	52
	LAPDSTTRSA	7	53
	LAKGTELKPA	8	54
	LAIIDATKNA	9	55
	LAVDGAQRSA	10	56
	PAPQDTTKKA	11	57
	LPHQDTTKNA	12	58
	LAKDATKTIA	13	59
	LAKQQSASTA	14	60
	LAKSDQSKPA	15	61

TABLE 1-continued

	Peptide No.	SEQID NO:	
	LSHQDTTKNA	16	62
5	LAANQPSKPA	17	63
	LAVSDSTKAA	18	64
	LAAQGTAKPA	19	65
	LAPDQTTTRNA	20	66
	LAASDSTKAA	21	67
	LAPQDTTTKNA	22	68
10	LAKADETRPA	23	69
	LAHQDTAKNA	24	70
	LAHQDTKKNA	25	71
	LAHQDTTKHA	26	72
	LAHQDTTKKA	27	73
	LAHQDTTTRNA	28	74
15	LAHQDTTTNA	29	75
	LAHQGTTKNA	30	76
	LAHQVTTKNA	31	77
	LAISDQSKPA	32	78
	LAKDATKTA	33	79
	LAKDTTKNA	34	80
20	LAKSDQSRPA	35	81
	LAPQDTTKNA	36	82
	LATSDSTKAA	37	83
	LAVDGSQRSA	38	84
	LPISDQTKHA	39	85
	LPKDATKTIA	40	86
25	LPPQDTTKNA	41	87
	PAPQDTTKNA	42	88
	QAHQDTTKNA	43	89
	LAHETSPRPA	44	90
	LAKSTSTAPA	45	91
	LADQDTTKNA	46	92
	LAESDQSKPA	47	93
30	LAHKDTTKNA	48	94
	LAHKTTQKQM	49	95
	LAHQDTTENA	50	96
	LAHQDTTINA	51	97
	LAHQDTTKKT	52	98
	LAHQDTTKND	53	99
35	LAHQDTTKNT	54	100
	LAHQDTTKNV	55	101
	LAHQDTTKTM	56	102
	LAHQNTTKNA	57	103
	LAHRDTTKNA	58	104
	LAISDQTNHA	59	105
40	LAKQKSASTA	60	106
	LAKSDQCKPA	61	107
	LAKSDQSKPD	62	108
	LAKSDQSNPA	63	109
	LAKSYQSKPA	64	110
	LANQDTTKNA	65	111
45	LAPQNTTKNA	66	112
	LAPSSIQKPA	67	113
	LAQQDTTKNA	68	114
	LAYQDTTKNA	69	115
	LDHQDTTKNA	70	116
	LDHQDTTKSA	71	117
	LGHQDTTKNA	72	118
50	LPHQDTTKND	73	119
	LPHQDTTKNT	74	120
	LPHQDTTNNA	75	121
	LTHQDTTKNA	76	122
	LTKDATKTIA	77	123
	LTPQDTTKNA	78	124
55	LVBHQDTTKNA	79	125
	LAKANQNTPA	80	126
	LATTPITKPA	81	127
	LATTPIAKPA	82	128
	LAIEDHTKSA	83	129
	LAQSEHQRP	84	130
	LAKSPNKDNA	85	131
60	LANQDYTKTA	86	132
	LANSTDQTRA	87	133
	LALGETTRPA	88	134
	LANSTEQTRA	89	135
	LAQADTTKNA	90	136
	LASKDITKTA	91	137
65	LASPRHNKCC	92	138
	LAHQDTTKTIA	93	139

41

TABLE 1-continued

	Peptide No.	SEQID NO:
LAAQGTANL	94	140
VAIEDHTKSA	95	141
LAKANQNTPKNA	96	142

The ability of the top 18 variants of the 96 variants depicted in Table 1 to infect the canine retina was further quantified using high throughput sequencing. Table 2 depicts the top 18 variants chosen for further quantification.

TABLE 2

LAKDATKNA	(SEQ ID NO: 47)
PAHQDTTKNA	(SEQ ID NO: 48)
LAHQDTTKNA	(SEQ ID NO: 49)
LATTSQNKPA	(SEQ ID NO: 50)
LAISDQTKHA	(SEQ ID NO: 51)
IARGVAPSSA	(SEQ ID NO: 52)
LAPDSTTRSA	(SEQ ID NO: 53)
LAKGTELKPA	(SEQ ID NO: 54)
LAIIDATKNA	(SEQ ID NO: 55)
LAVDGAQRSA	(SEQ ID NO: 56)
PAPQDTTKKA	(SEQ ID NO: 57)
LPHQDTTKNA	(SEQ ID NO: 58)
LAKDATKTIA	(SEQ ID NO: 59)
LAKQQSASTA	(SEQ ID NO: 60)
LAKSDQSKPA	(SEQ ID NO: 61)

42

TABLE 2-continued

LSHQDTTKNA	(SEQ ID NO: 62)
LAANQPSKPA	(SEQ ID NO: 63)
LAVSDSTKAA	(SEQ ID NO: 64)

Eighteen variants were packaged with a ubiquitous CAG promoter driving expression of GFP. The GFP cDNA was fused to a unique 25 base-pair bar code identifier. Each of the 18 variants was packaged with a unique GFP barcode. Packaged variants were mixed in equal ratios and injected into the retina, along with control AAV2-based vectors (negative controls representing the naturally occurring parental serotype). After injection, DNA and mRNA were collected from photoreceptor and RPE cells. DNA and mRNA levels were quantified to determine the ability of the canine-derived vectors to deliver DNA to the retina and lead to transgene expression (FIG. 2).

FIG. 2. Deep sequencing of variants containing GFP-barcode constructs. Infection of the canine retina by the canine-derived variants was quantified by deep sequencing of tagged GFP cDNA and mRNA.

Expression of the 18-member library was imaged using confocal microscopy of frozen retinal sections. GFP expression showed that retinal cells in the inner retina, and photoreceptors in the outer retina were targeted with the 18-member library (FIG. 3).

FIG. 3. The 18-member canine-derived AAV variant library infects cells in the ganglion cell layer, the inner nuclear layer, the photoreceptor layer, and the RPE layer.

Of the top 18 variants tested, 2 variants led to highest level of DNA and mRNA recovery. The variant leading to the highest level of DNA recovery had the insertion sequence ~588-PAPQDTTKKA (SEQ ID NO:57). The variant leading to the highest level of mRNA expression had the insertion sequence ~588-LAPDSTTRSA (SEQ ID NO:53).

While the present invention has been described with reference to the specific embodiments thereof, it should be understood by those skilled in the art that various changes may be made and equivalents may be substituted without departing from the true spirit and scope of the invention. In addition, many modifications may be made to adapt a particular situation, material, composition of matter, process, process step or steps, to the objective, spirit and scope of the present invention. All such modifications are intended to be within the scope of the claims appended hereto.

## SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 152

<210> SEQ ID NO 1

<211> LENGTH: 733

<212> TYPE: PRT

<213> ORGANISM: Adeno-associated virus-2

<400> SEQUENCE: 1

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser  
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro  
20 25 30

-continued

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Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro  
                   35                                  40                                  45  
  
 Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro  
           50                                  55                                  60  
  
 Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp  
   65                                  70                                  75                                  80  
  
 Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala  
                   85                                  90                                  95  
  
 Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly  
                   100                                  105                                  110  
  
 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro  
           115                                  120                                  125  
  
 Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg  
   130                                  135                                  140  
  
 Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly  
   145                                  150                                  155                                  160  
  
 Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr  
                   165                                  170                                  175  
  
 Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro  
                   180                                  185                                  190  
  
 Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly  
                   195                                  200                                  205  
  
 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser  
   210                                  215                                  220  
  
 Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile  
   225                                  230                                  235                                  240  
  
 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu  
                   245                                  250                                  255  
  
 Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr  
                   260                                  265                                  270  
  
 Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His  
                   275                                  280                                  285  
  
 Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp  
                   290                                  295                                  300  
  
 Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val  
   305                                  310                                  315                                  320  
  
 Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu  
                   325                                  330                                  335  
  
 Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr  
                   340                                  345                                  350  
  
 Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp  
                   355                                  360                                  365  
  
 Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser  
   370                                  375                                  380  
  
 Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser  
   385                                  390                                  395                                  400  
  
 Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu  
                   405                                  410                                  415  
  
 Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg  
                   420                                  425                                  430  
  
 Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr  
                   435                                  440                                  445  
  
 Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln

-continued

450	455	460
Ala Gly Ala Ser Asp 465	Ile Arg Asp Gln Ser 470	Arg Asn Trp Leu Pro Gly 475 480
Pro Cys Tyr Arg 485	Gln Gln Arg Val Ser Lys Thr 490	Ser Ala Asp Asn Asn 495
Asn Ser Glu Tyr Ser 500	Trp Thr Gly Ala Thr Lys Tyr His 505	Leu Asn Gly 510
Arg Asp Ser Leu Val 515	Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp 520 525	
Asp Glu Glu Lys Phe Phe 530	Pro Gln Ser Gly Val Leu Ile Phe Gly Lys 535 540	
Gln Gly Ser Glu Lys 545	Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr 550 555 560	
Asp Glu Glu Glu Ile Arg Thr Thr 565	Asn Pro Val Ala Thr Glu Gln Tyr 570 575	
Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr 580	585	590
Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp 595	600	605
Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr 610	615	620
Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys 625	630	635 640
His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn 645	650	655
Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln 660	665	670
Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys 675	680	685
Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr 690	695	700
Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr 705	710	715 720
Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg 725	730	

<210> SEQ ID NO 2  
 <211> LENGTH: 42  
 <212> TYPE: PRT  
 <213> ORGANISM: Adeno-associated virus-2

<400> SEQUENCE: 2

Pro Val Ala Thr Glu Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg 1 5 10 15
Gly Asn Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu 20 25 30
Pro Gly Met Val Trp Gln Asp Arg Asp Val 35 40

<210> SEQ ID NO 3  
 <211> LENGTH: 42  
 <212> TYPE: PRT  
 <213> ORGANISM: Adeno-associated virus-1

<400> SEQUENCE: 3

Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser



-continued

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1                    5                    10                    15

Ser Ser Thr Asp Pro Ala Thr Gly Asp Val His Ala Met Gly Ala Leu  
                  20                    25                    30

Pro Gly Met Val Trp Gln Asp Arg Asp Val  
                  35                    40

<210> SEQ ID NO 4  
 <211> LENGTH: 42  
 <212> TYPE: PRT  
 <213> ORGANISM: Adeno-associated virus-5

<400> SEQUENCE: 4

Arg Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser  
1                    5                    10                    15

Ser Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val  
                  20                    25                    30

Pro Gly Ser Val Trp Met Glu Arg Asp Val  
                  35                    40

<210> SEQ ID NO 5  
 <211> LENGTH: 42  
 <212> TYPE: PRT  
 <213> ORGANISM: Adeno-associated virus-6

<400> SEQUENCE: 5

Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Leu Gln Ser  
1                    5                    10                    15

Ser Ser Thr Asp Pro Ala Thr Gly Asp Val His Val Met Gly Ala Leu  
                  20                    25                    30

Pro Gly Met Val Trp Gln Asp Arg Asp Val  
                  35                    40

<210> SEQ ID NO 6  
 <211> LENGTH: 42  
 <212> TYPE: PRT  
 <213> ORGANISM: Adeno-associated virus-7

<400> SEQUENCE: 6

Pro Val Ala Thr Glu Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala  
1                    5                    10                    15

Ala Asn Thr Ala Ala Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu  
                  20                    25                    30

Pro Gly Met Val Trp Gln Asn Arg Asp Val  
                  35                    40

<210> SEQ ID NO 7  
 <211> LENGTH: 42  
 <212> TYPE: PRT  
 <213> ORGANISM: Adeno-associated virus-8

<400> SEQUENCE: 7

Pro Val Ala Thr Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln  
1                    5                    10                    15

Gln Asn Thr Ala Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu  
                  20                    25                    30

Pro Gly Met Val Trp Gln Asn Arg Asp Val  
                  35                    40

<210> SEQ ID NO 8  
 <211> LENGTH: 42

-continued

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<212> TYPE: PRT  
 <213> ORGANISM: Adeno-associated virus-9  
 <400> SEQUENCE: 8

Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln Ser  
 1 5 10 15  
 Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu  
 20 25 30  
 Pro Gly Met Val Trp Gln Asp Arg Asp Val  
 35 40

<210> SEQ ID NO 9  
 <211> LENGTH: 42  
 <212> TYPE: PRT  
 <213> ORGANISM: Adeno-associated virus-10

<400> SEQUENCE: 9

Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln  
 1 5 10 15  
 Ala Asn Thr Gly Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu  
 20 25 30  
 Pro Gly Met Val Trp Gln Asn Arg Asp Val  
 35 40

<210> SEQ ID NO 10  
 <211> LENGTH: 224  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

Met Ser Arg Lys Ile Glu Gly Phe Leu Leu Leu Leu Leu Phe Gly Tyr  
 1 5 10 15  
 Glu Ala Thr Leu Gly Leu Ser Ser Thr Glu Asp Glu Gly Glu Asp Pro  
 20 25 30  
 Trp Tyr Gln Lys Ala Cys Lys Cys Asp Cys Gln Gly Gly Pro Asn Ala  
 35 40 45  
 Leu Trp Ser Ala Gly Ala Thr Ser Leu Asp Cys Ile Pro Glu Cys Pro  
 50 55 60  
 Tyr His Lys Pro Leu Gly Phe Glu Ser Gly Glu Val Thr Pro Asp Gln  
 65 70 75 80  
 Ile Thr Cys Ser Asn Pro Glu Gln Tyr Val Gly Trp Tyr Ser Ser Trp  
 85 90 95  
 Thr Ala Asn Lys Ala Arg Leu Asn Ser Gln Gly Phe Gly Cys Ala Trp  
 100 105 110  
 Leu Ser Lys Phe Gln Asp Ser Ser Gln Trp Leu Gln Ile Asp Leu Lys  
 115 120 125  
 Glu Ile Lys Val Ile Ser Gly Ile Leu Thr Gln Gly Arg Cys Asp Ile  
 130 135 140  
 Asp Glu Trp Met Thr Lys Tyr Ser Val Gln Tyr Arg Thr Asp Glu Arg  
 145 150 155 160  
 Leu Asn Trp Ile Tyr Tyr Lys Asp Gln Thr Gly Asn Asn Arg Val Phe  
 165 170 175  
 Tyr Gly Asn Ser Asp Arg Thr Ser Thr Val Gln Asn Leu Leu Arg Pro  
 180 185 190  
 Pro Ile Ile Ser Arg Phe Ile Arg Leu Ile Pro Leu Gly Trp His Val  
 195 200 205  
 Arg Ile Ala Ile Arg Met Glu Leu Leu Glu Cys Val Ser Lys Cys Ala

-continued

210                                    215                                    220

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<210> SEQ ID NO 11  
 <211> LENGTH: 247  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys Met  
 1                                    5                                    10                                    15

Lys Ala Ala Pro Met Lys Glu Ala Asn Ile Arg Gly Gln Gly Gly Leu  
                                   20                                    25                                    30

Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu Glu Ser Val Asn Gly  
                                   35                                    40                                    45

Pro Lys Ala Gly Ser Arg Gly Leu Thr Ser Leu Ala Asp Thr Phe Glu  
  50                                    55                                    60

His Val Ile Glu Glu Leu Leu Asp Glu Asp His Lys Val Arg Pro Asn  
 65                                    70                                    75                                    80

Glu Glu Asn Asn Lys Asp Ala Asp Leu Tyr Thr Ser Arg Val Met Leu  
                                   85                                    90                                    95

Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu Leu Glu Glu  
                                   100                                    105                                    110

Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Met Val Leu Arg  
                                   115                                    120                                    125

His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys Asp Ser Ile  
  130                                    135                                    140

Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val Asp Met Ser  
 145                                    150                                    155                                    160

Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys Gly Gln  
                                   165                                    170                                    175

Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly Tyr Thr  
                                   180                                    185                                    190

Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser Gln Cys  
  195                                    200                                    205

Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser Lys Lys  
  210                                    215                                    220

Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val Cys Thr  
 225                                    230                                    235                                    240

Leu Thr Ile Lys Arg Gly Arg  
                                   245

<210> SEQ ID NO 12  
 <211> LENGTH: 533  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

Met Ser Ile Gln Val Glu His Pro Ala Gly Gly Tyr Lys Lys Leu Phe  
 1                                    5                                    10                                    15

Glu Thr Val Glu Glu Leu Ser Ser Pro Leu Thr Ala His Val Thr Gly  
                                   20                                    25                                    30

Arg Ile Pro Leu Trp Leu Thr Gly Ser Leu Leu Arg Cys Gly Pro Gly  
                                   35                                    40                                    45

Leu Phe Glu Val Gly Ser Glu Pro Phe Tyr His Leu Phe Asp Gly Gln  
  50                                    55                                    60

Ala Leu Leu His Lys Phe Asp Phe Lys Glu Gly His Val Thr Tyr His

-continued

65	70	75	80
Arg Arg Phe Ile Arg Thr Asp Ala Tyr Val Arg Ala Met Thr Glu Lys 85 90 95			
Arg Ile Val Ile Thr Glu Phe Gly Thr Cys Ala Phe Pro Asp Pro Cys 100 105 110			
Lys Asn Ile Phe Ser Arg Phe Phe Ser Tyr Phe Arg Gly Val Glu Val 115 120 125			
Thr Asp Asn Ala Leu Val Asn Val Tyr Pro Val Gly Glu Asp Tyr Tyr 130 135 140			
Ala Cys Thr Glu Thr Asn Phe Ile Thr Lys Ile Asn Pro Glu Thr Leu 145 150 155 160			
Glu Thr Ile Lys Gln Val Asp Leu Cys Asn Tyr Val Ser Val Asn Gly 165 170 175			
Ala Thr Ala His Pro His Ile Glu Asn Asp Gly Thr Val Tyr Asn Ile 180 185 190			
Gly Asn Cys Phe Gly Lys Asn Phe Ser Ile Ala Tyr Asn Ile Val Lys 195 200 205			
Ile Pro Pro Leu Gln Ala Asp Lys Glu Asp Pro Ile Ser Lys Ser Glu 210 215 220			
Ile Val Val Gln Phe Pro Cys Ser Asp Arg Phe Lys Pro Ser Tyr Val 225 230 235 240			
His Ser Phe Gly Leu Thr Pro Asn Tyr Ile Val Phe Val Glu Thr Pro 245 250 255			
Val Lys Ile Asn Leu Phe Lys Phe Leu Ser Ser Trp Ser Leu Trp Gly 260 265 270			
Ala Asn Tyr Met Asp Cys Phe Glu Ser Asn Glu Thr Met Gly Val Trp 275 280 285			
Leu His Ile Ala Asp Lys Lys Arg Lys Lys Tyr Leu Asn Asn Lys Tyr 290 295 300			
Arg Thr Ser Pro Phe Asn Leu Phe His His Ile Asn Thr Tyr Glu Asp 305 310 315 320			
Asn Gly Phe Leu Ile Val Asp Leu Cys Cys Trp Lys Gly Phe Glu Phe 325 330 335			
Val Tyr Asn Tyr Leu Tyr Leu Ala Asn Leu Arg Glu Asn Trp Glu Glu 340 345 350			
Val Lys Lys Asn Ala Arg Lys Ala Pro Gln Pro Glu Val Arg Arg Tyr 355 360 365			
Val Leu Pro Leu Asn Ile Asp Lys Ala Asp Thr Gly Lys Asn Leu Val 370 375 380			
Thr Leu Pro Asn Thr Thr Ala Thr Ala Ile Leu Cys Ser Asp Glu Thr 385 390 395 400			
Ile Trp Leu Glu Pro Glu Val Leu Phe Ser Gly Pro Arg Gln Ala Phe 405 410 415			
Glu Phe Pro Gln Ile Asn Tyr Gln Lys Tyr Cys Gly Lys Pro Tyr Thr 420 425 430			
Tyr Ala Tyr Gly Leu Gly Leu Asn His Phe Val Pro Asp Arg Leu Cys 435 440 445			
Lys Leu Asn Val Lys Thr Lys Glu Thr Trp Val Trp Gln Glu Pro Asp 450 455 460			
Ser Tyr Pro Ser Glu Pro Ile Phe Val Ser His Pro Asp Ala Leu Glu 465 470 475 480			
Glu Asp Asp Gly Val Val Leu Ser Val Val Val Ser Pro Gly Ala Gly 485 490 495			

-continued

Gln Lys Pro Ala Tyr Leu Leu Ile Leu Asn Ala Lys Asp Leu Ser Glu  
500 505 510

Val Ala Arg Ala Glu Val Glu Ile Asn Ile Pro Val Thr Phe His Gly  
515 520 525

Leu Phe Lys Lys Ser  
530

<210> SEQ ID NO 13

<211> LENGTH: 346

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 13

Met Ala Leu Leu Lys Val Lys Phe Asp Gln Lys Lys Arg Val Lys Leu  
1 5 10 15

Ala Gln Gly Leu Trp Leu Met Asn Trp Phe Ser Val Leu Ala Gly Ile  
20 25 30

Ile Ile Phe Ser Leu Gly Leu Phe Leu Lys Ile Glu Leu Arg Lys Arg  
35 40 45

Ser Asp Val Met Asn Asn Ser Glu Ser His Phe Val Pro Asn Ser Leu  
50 55 60

Ile Gly Met Gly Val Leu Ser Cys Val Phe Asn Ser Leu Ala Gly Lys  
65 70 75 80

Ile Cys Tyr Asp Ala Leu Asp Pro Ala Lys Tyr Ala Arg Trp Lys Pro  
85 90 95

Trp Leu Lys Pro Tyr Leu Ala Ile Cys Val Leu Phe Asn Ile Ile Leu  
100 105 110

Phe Leu Val Ala Leu Cys Cys Phe Leu Leu Arg Gly Ser Leu Glu Asn  
115 120 125

Thr Leu Gly Gln Gly Leu Lys Asn Gly Met Lys Tyr Tyr Arg Asp Thr  
130 135 140

Asp Thr Pro Gly Arg Cys Phe Met Lys Lys Thr Ile Asp Met Leu Gln  
145 150 155 160

Ile Glu Phe Lys Cys Cys Gly Asn Asn Gly Phe Arg Asp Trp Phe Glu  
165 170 175

Ile Gln Trp Ile Ser Asn Arg Tyr Leu Asp Phe Ser Ser Lys Glu Val  
180 185 190

Lys Asp Arg Ile Lys Ser Asn Val Asp Gly Arg Tyr Leu Val Asp Gly  
195 200 205

Val Pro Phe Ser Cys Cys Asn Pro Ser Ser Pro Arg Pro Cys Ile Gln  
210 215 220

Tyr Gln Ile Thr Asn Asn Ser Ala His Tyr Ser Tyr Asp His Gln Thr  
225 230 235 240

Glu Glu Leu Asn Leu Trp Val Arg Gly Cys Arg Ala Ala Leu Leu Ser  
245 250 255

Tyr Tyr Ser Ser Leu Met Asn Ser Met Gly Val Val Thr Leu Leu Ile  
260 265 270

Trp Leu Phe Glu Val Thr Ile Thr Ile Gly Leu Arg Tyr Leu Gln Thr  
275 280 285

Ser Leu Asp Gly Val Ser Asn Pro Glu Glu Ser Glu Ser Glu Ser Gln  
290 295 300

Gly Trp Leu Leu Glu Arg Ser Val Pro Glu Thr Trp Lys Ala Phe Leu  
305 310 315 320

Glu Ser Val Lys Lys Leu Gly Lys Gly Asn Gln Val Glu Ala Glu Gly

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	325		330		335
Ala Asp Ala Gly Gln Ala Pro Glu Ala Gly					
	340		345		
<p>&lt;210&gt; SEQ ID NO 14          &lt;211&gt; LENGTH: 470          &lt;212&gt; TYPE: PRT          &lt;213&gt; ORGANISM: Homo sapiens</p> <p>&lt;400&gt; SEQUENCE: 14</p>					
Met Ser His His Pro Ser Gly Leu Arg Ala Gly Phe Ser Ser Thr Ser					
1	5		10		15
Tyr Arg Arg Thr Phe Gly Pro Pro Pro Ser Leu Ser Pro Gly Ala Phe					
	20		25		30
Ser Tyr Ser Ser Ser Ser Arg Phe Ser Ser Ser Arg Leu Leu Gly Ser					
	35		40		45
Ala Ser Pro Ser Ser Ser Val Arg Leu Gly Ser Phe Arg Ser Pro Arg					
	50		55		60
Ala Gly Ala Gly Ala Leu Leu Arg Leu Pro Ser Glu Arg Leu Asp Phe					
65		70		75	80
Ser Met Ala Glu Ala Leu Asn Gln Glu Phe Leu Ala Thr Arg Ser Asn					
	85		90		95
Glu Lys Gln Glu Leu Gln Glu Leu Asn Asp Arg Phe Ala Asn Phe Ile					
	100		105		110
Glu Lys Val Arg Phe Leu Glu Gln Gln Asn Ala Ala Leu Arg Gly Glu					
	115		120		125
Leu Ser Gln Ala Arg Gly Gln Glu Pro Ala Arg Ala Asp Gln Leu Cys					
	130		135		140
Gln Gln Glu Leu Arg Glu Leu Arg Arg Glu Leu Glu Leu Leu Gly Arg					
145		150		155	160
Glu Arg Asp Arg Val Gln Val Glu Arg Asp Gly Leu Ala Glu Asp Leu					
	165		170		175
Ala Ala Leu Lys Gln Arg Leu Glu Glu Glu Thr Arg Lys Arg Glu Asp					
	180		185		190
Ala Glu His Asn Leu Val Leu Phe Arg Lys Asp Val Asp Asp Ala Thr					
	195		200		205
Leu Ser Arg Leu Glu Leu Glu Arg Lys Ile Glu Ser Leu Met Asp Glu					
	210		215		220
Ile Glu Phe Leu Lys Lys Leu His Glu Glu Glu Leu Arg Asp Leu Gln					
225		230		235	240
Val Ser Val Glu Ser Gln Gln Val Gln Gln Val Glu Val Glu Ala Thr					
	245		250		255
Val Lys Pro Glu Leu Thr Ala Ala Leu Arg Asp Ile Arg Ala Gln Tyr					
	260		265		270
Glu Ser Ile Ala Ala Lys Asn Leu Gln Glu Ala Glu Glu Trp Tyr Lys					
	275		280		285
Ser Lys Tyr Ala Asp Leu Ser Asp Ala Ala Asn Arg Asn His Glu Ala					
	290		295		300
Leu Arg Gln Ala Lys Gln Glu Met Asn Glu Ser Arg Arg Gln Ile Gln					
305		310		315	320
Ser Leu Thr Cys Glu Val Asp Gly Leu Arg Gly Thr Asn Glu Ala Leu					
	325		330		335
Leu Arg Gln Leu Arg Glu Leu Glu Glu Gln Phe Ala Leu Glu Ala Gly					
	340		345		350

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Gly Tyr Gln Ala Gly Ala Ala Arg Leu Glu Glu Glu Leu Arg Gln Leu  
 355 360 365

Lys Glu Glu Met Ala Arg His Leu Arg Glu Tyr Gln Glu Leu Leu Asn  
 370 375 380

Val Lys Met Ala Leu Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu  
 385 390 395 400

Glu Gly Glu Glu Ser Arg Ile Ser Val Pro Val His Ser Phe Ala Ser  
 405 410 415

Leu Asn Ile Lys Thr Thr Val Pro Glu Val Glu Pro Pro Gln Asp Ser  
 420 425 430

His Ser Arg Lys Thr Val Leu Ile Lys Thr Ile Glu Thr Arg Asn Gly  
 435 440 445

Glu Val Val Thr Glu Ser Gln Lys Glu Gln Arg Ser Glu Leu Asp Lys  
 450 455 460

Ser Ser Ala His Ser Tyr  
 465 470

<210> SEQ ID NO 15  
 <211> LENGTH: 1286  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

Met Ser His Leu Val Asp Pro Thr Ser Gly Asp Leu Pro Val Arg Asp  
 1 5 10 15

Ile Asp Ala Ile Pro Leu Val Leu Pro Ala Ser Lys Gly Lys Asn Met  
 20 25 30

Lys Thr Gln Pro Pro Leu Ser Arg Met Asn Arg Glu Glu Leu Glu Asp  
 35 40 45

Ser Phe Phe Arg Leu Arg Glu Asp His Met Leu Val Lys Glu Leu Ser  
 50 55 60

Trp Lys Gln Gln Asp Glu Ile Lys Arg Leu Arg Thr Thr Leu Leu Arg  
 65 70 75 80

Leu Thr Ala Ala Gly Arg Asp Leu Arg Val Ala Glu Glu Ala Ala Pro  
 85 90 95

Leu Ser Glu Thr Ala Arg Arg Gly Gln Lys Ala Gly Trp Arg Gln Arg  
 100 105 110

Leu Ser Met His Gln Arg Pro Gln Met His Arg Leu Gln Gly His Phe  
 115 120 125

His Cys Val Gly Pro Ala Ser Pro Arg Arg Ala Gln Pro Arg Val Gln  
 130 135 140

Val Gly His Arg Gln Leu His Thr Ala Gly Ala Pro Val Pro Glu Lys  
 145 150 155 160

Pro Lys Arg Gly Pro Arg Asp Arg Leu Ser Tyr Thr Ala Pro Pro Ser  
 165 170 175

Phe Lys Glu His Ala Thr Asn Glu Asn Arg Gly Glu Val Ala Ser Lys  
 180 185 190

Pro Ser Glu Leu Val Ser Gly Ser Asn Ser Ile Ile Ser Phe Ser Ser  
 195 200 205

Val Ile Ser Met Ala Lys Pro Ile Gly Leu Cys Met Pro Asn Ser Ala  
 210 215 220

His Ile Met Ala Ser Asn Thr Met Gln Val Glu Glu Pro Pro Lys Ser  
 225 230 235 240

Pro Glu Lys Met Trp Pro Lys Asp Glu Asn Phe Glu Gln Arg Ser Ser  
 245 250 255

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Leu Glu Cys Ala Gln Lys Ala Ala Glu Leu Arg Ala Ser Ile Lys Glu  
 260 265 270  
 Lys Val Glu Leu Ile Arg Leu Lys Lys Leu Leu His Glu Arg Asn Ala  
 275 280 285  
 Ser Leu Val Met Thr Lys Ala Gln Leu Thr Glu Val Gln Glu Ala Tyr  
 290 295 300  
 Glu Thr Leu Leu Gln Lys Asn Gln Gly Ile Leu Ser Ala Ala His Glu  
 305 310 315 320  
 Ala Leu Leu Lys Gln Val Asn Glu Leu Arg Ala Glu Leu Lys Glu Glu  
 325 330 335  
 Ser Lys Lys Ala Val Ser Leu Lys Ser Gln Leu Glu Asp Val Ser Ile  
 340 345 350  
 Leu Gln Met Thr Leu Lys Glu Phe Gln Glu Arg Val Glu Asp Leu Glu  
 355 360 365  
 Lys Glu Arg Lys Leu Leu Asn Asp Asn Tyr Asp Lys Leu Leu Glu Ser  
 370 375 380  
 Met Leu Asp Ser Ser Asp Ser Ser Ser Gln Pro His Trp Ser Asn Glu  
 385 390 395 400  
 Leu Ile Ala Glu Gln Leu Gln Gln Gln Val Ser Gln Leu Gln Asp Gln  
 405 410 415  
 Leu Asp Ala Glu Leu Glu Asp Lys Arg Lys Val Leu Leu Glu Leu Ser  
 420 425 430  
 Arg Glu Lys Ala Gln Asn Glu Asp Leu Lys Leu Glu Val Thr Asn Ile  
 435 440 445  
 Leu Gln Lys His Lys Gln Glu Val Glu Leu Leu Gln Asn Ala Ala Thr  
 450 455 460  
 Ile Ser Gln Pro Pro Asp Arg Gln Ser Glu Pro Ala Thr His Pro Ala  
 465 470 475 480  
 Val Leu Gln Glu Asn Thr Gln Ile Glu Pro Ser Glu Pro Lys Asn Gln  
 485 490 495  
 Glu Glu Lys Lys Leu Ser Gln Val Leu Asn Glu Leu Gln Val Ser His  
 500 505 510  
 Ala Glu Thr Thr Leu Glu Leu Glu Lys Thr Arg Asp Met Leu Ile Leu  
 515 520 525  
 Gln Arg Lys Ile Asn Val Cys Tyr Gln Glu Glu Leu Glu Ala Met Met  
 530 535 540  
 Thr Lys Ala Asp Asn Asp Asn Arg Asp His Lys Glu Lys Leu Glu Arg  
 545 550 555 560  
 Leu Thr Arg Leu Leu Asp Leu Lys Asn Asn Arg Ile Lys Gln Leu Glu  
 565 570 575  
 Gly Ile Leu Arg Ser His Asp Leu Pro Thr Ser Glu Gln Leu Lys Asp  
 580 585 590  
 Val Ala Tyr Gly Thr Arg Pro Leu Ser Leu Cys Leu Glu Thr Leu Pro  
 595 600 605  
 Ala His Gly Asp Glu Asp Lys Val Asp Ile Ser Leu Leu His Gln Gly  
 610 615 620  
 Glu Asn Leu Phe Glu Leu His Ile His Gln Ala Phe Leu Thr Ser Ala  
 625 630 635 640  
 Ala Leu Ala Gln Ala Gly Asp Thr Gln Pro Thr Thr Phe Cys Thr Tyr  
 645 650 655  
 Ser Phe Tyr Asp Phe Glu Thr His Cys Thr Pro Leu Ser Val Gly Pro  
 660 665 670



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Gln Pro Leu Tyr Asp Phe Thr Ser Gln Tyr Val Met Glu Thr Asp Ser  
 675 680 685  
 Leu Phe Leu His Tyr Leu Gln Glu Ala Ser Ala Arg Leu Asp Ile His  
 690 695 700  
 Gln Ala Met Ala Ser Glu His Ser Thr Leu Ala Ala Gly Trp Ile Cys  
 705 710 715 720  
 Phe Asp Arg Val Leu Glu Thr Val Glu Lys Val His Gly Leu Ala Thr  
 725 730 735  
 Leu Ile Gly Ala Gly Gly Glu Glu Phe Gly Val Leu Glu Tyr Trp Met  
 740 745 750  
 Arg Leu Arg Phe Pro Ile Lys Pro Ser Leu Gln Ala Cys Asn Lys Arg  
 755 760 765  
 Lys Lys Ala Gln Val Tyr Leu Ser Thr Asp Val Leu Gly Gly Arg Lys  
 770 775 780  
 Ala Gln Glu Glu Glu Phe Arg Ser Glu Ser Trp Glu Pro Gln Asn Glu  
 785 790 795 800  
 Leu Trp Ile Glu Ile Thr Lys Cys Cys Gly Leu Arg Ser Arg Trp Leu  
 805 810 815  
 Gly Thr Gln Pro Ser Pro Tyr Ala Val Tyr Arg Phe Phe Thr Phe Ser  
 820 825 830  
 Asp His Asp Thr Ala Ile Ile Pro Ala Ser Asn Asn Pro Tyr Phe Arg  
 835 840 845  
 Asp Gln Ala Arg Phe Pro Val Leu Val Thr Ser Asp Leu Asp His Tyr  
 850 855 860  
 Leu Arg Arg Glu Ala Leu Ser Ile His Val Phe Asp Asp Glu Asp Leu  
 865 870 875 880  
 Glu Pro Gly Ser Tyr Leu Gly Arg Ala Arg Val Pro Leu Leu Pro Leu  
 885 890 895  
 Ala Lys Asn Glu Ser Ile Lys Gly Asp Phe Asn Leu Thr Asp Pro Ala  
 900 905 910  
 Glu Lys Pro Asn Gly Ser Ile Gln Val Gln Leu Asp Trp Lys Phe Pro  
 915 920 925  
 Tyr Ile Pro Pro Glu Ser Phe Leu Lys Pro Glu Ala Gln Thr Lys Gly  
 930 935 940  
 Lys Asp Thr Lys Asp Ser Ser Lys Ile Ser Ser Glu Glu Glu Lys Ala  
 945 950 955 960  
 Ser Phe Pro Ser Gln Asp Gln Met Ala Ser Pro Glu Val Pro Ile Glu  
 965 970 975  
 Ala Gly Gln Tyr Arg Ser Lys Arg Lys Pro Pro His Gly Gly Glu Arg  
 980 985 990  
 Lys Glu Lys Glu His Gln Val Val Ser Tyr Ser Arg Arg Lys His Gly  
 995 1000 1005  
 Lys Arg Ile Gly Val Gln Gly Lys Asn Arg Met Glu Tyr Leu Ser  
 1010 1015 1020  
 Leu Asn Ile Leu Asn Gly Asn Thr Pro Glu Gln Val Asn Tyr Thr  
 1025 1030 1035  
 Glu Trp Lys Phe Ser Glu Thr Asn Ser Phe Ile Gly Asp Gly Phe  
 1040 1045 1050  
 Lys Asn Gln His Glu Glu Glu Glu Met Thr Leu Ser His Ser Ala  
 1055 1060 1065  
 Leu Lys Gln Lys Glu Pro Leu His Pro Val Asn Asp Lys Glu Ser  
 1070 1075 1080  
 Ser Glu Gln Gly Ser Glu Val Ser Glu Ala Gln Thr Thr Asp Ser

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1085	1090	1095
Asp Asp Val Ile Val Pro Pro Met Ser Gln Lys Tyr Pro Lys Ala 1100 1105 1110		
Asp Ser Glu Lys Met Cys Ile Glu Ile Val Ser Leu Ala Phe Tyr 1115 1120 1125		
Pro Glu Ala Glu Val Met Ser Asp Glu Asn Ile Lys Gln Val Tyr 1130 1135 1140		
Val Glu Tyr Lys Phe Tyr Asp Leu Pro Leu Ser Glu Thr Glu Thr 1145 1150 1155		
Pro Val Ser Leu Arg Lys Pro Arg Ala Gly Glu Glu Ile His Phe 1160 1165 1170		
His Phe Ser Lys Val Ile Asp Leu Asp Pro Gln Glu Gln Gln Gly 1175 1180 1185		
Arg Arg Arg Phe Leu Phe Asp Met Leu Asn Gly Gln Asp Pro Asp 1190 1195 1200		
Gln Gly His Leu Lys Phe Thr Val Val Ser Asp Pro Leu Asp Glu 1205 1210 1215		
Glu Lys Lys Glu Cys Glu Glu Val Gly Tyr Ala Tyr Leu Gln Leu 1220 1225 1230		
Trp Gln Ile Leu Glu Ser Gly Arg Asp Ile Leu Glu Gln Glu Leu 1235 1240 1245		
Asp Ile Val Ser Pro Glu Asp Leu Ala Thr Pro Ile Gly Arg Leu 1250 1255 1260		
Lys Val Ser Leu Gln Ala Ala Ala Val Leu His Ala Ile Tyr Lys 1265 1270 1275		
Glu Met Thr Glu Asp Leu Phe Ser 1280 1285		

&lt;210&gt; SEQ ID NO 16

&lt;211&gt; LENGTH: 653

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 16

Met Ala Asp Thr Leu Pro Ser Glu Phe Asp Val Ile Val Ile Gly Thr 1 5 10 15
Gly Leu Pro Glu Ser Ile Ile Ala Ala Ala Cys Ser Arg Ser Gly Arg 20 25 30
Arg Val Leu His Val Asp Ser Arg Ser Tyr Tyr Gly Gly Asn Trp Ala 35 40 45
Ser Phe Ser Phe Ser Gly Leu Leu Ser Trp Leu Lys Glu Tyr Gln Glu 50 55 60
Asn Ser Asp Ile Val Ser Asp Ser Pro Val Trp Gln Asp Gln Ile Leu 65 70 75 80
Glu Asn Glu Glu Ala Ile Ala Leu Ser Arg Lys Asp Lys Thr Ile Gln 85 90 95
His Val Glu Val Phe Cys Tyr Ala Ser Gln Asp Leu His Glu Asp Val 100 105 110
Glu Glu Ala Gly Ala Leu Gln Lys Asn His Ala Leu Val Thr Ser Ala 115 120 125
Asn Ser Thr Glu Ala Ala Asp Ser Ala Phe Leu Pro Thr Glu Asp Glu 130 135 140
Ser Leu Ser Thr Met Ser Cys Glu Met Leu Thr Glu Gln Thr Pro Ser 145 150 155 160

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Ser	Asp	Pro	Glu	Asn	Ala	Leu	Glu	Val	Asn	Gly	Ala	Glu	Val	Thr	Gly
				165					170					175	
Glu	Lys	Glu	Asn	His	Cys	Asp	Asp	Lys	Thr	Cys	Val	Pro	Ser	Thr	Ser
			180					185					190		
Ala	Glu	Asp	Met	Ser	Glu	Asn	Val	Pro	Ile	Ala	Glu	Asp	Thr	Thr	Glu
		195					200					205			
Gln	Pro	Lys	Lys	Asn	Arg	Ile	Thr	Tyr	Ser	Gln	Ile	Ile	Lys	Glu	Gly
	210					215					220				
Arg	Arg	Phe	Asn	Ile	Asp	Leu	Val	Ser	Lys	Leu	Leu	Tyr	Ser	Arg	Gly
225					230					235					240
Leu	Leu	Ile	Asp	Leu	Leu	Ile	Lys	Ser	Asn	Val	Ser	Arg	Tyr	Ala	Glu
				245					250					255	
Phe	Lys	Asn	Ile	Thr	Arg	Ile	Leu	Ala	Phe	Arg	Glu	Gly	Arg	Val	Glu
			260					265					270		
Gln	Val	Pro	Cys	Ser	Arg	Ala	Asp	Val	Phe	Asn	Ser	Lys	Gln	Leu	Thr
		275					280					285			
Met	Val	Glu	Lys	Arg	Met	Leu	Met	Lys	Phe	Leu	Thr	Phe	Cys	Met	Glu
	290					295					300				
Tyr	Glu	Lys	Tyr	Pro	Asp	Glu	Tyr	Lys	Gly	Tyr	Glu	Glu	Ile	Thr	Phe
305					310					315					320
Tyr	Glu	Tyr	Leu	Lys	Thr	Gln	Lys	Leu	Thr	Pro	Asn	Leu	Gln	Tyr	Ile
				325					330					335	
Val	Met	His	Ser	Ile	Ala	Met	Thr	Ser	Glu	Thr	Ala	Ser	Ser	Thr	Ile
			340					345					350		
Asp	Gly	Leu	Lys	Ala	Thr	Lys	Asn	Phe	Leu	His	Cys	Leu	Gly	Arg	Tyr
		355					360					365			
Gly	Asn	Thr	Pro	Phe	Leu	Phe	Pro	Leu	Tyr	Gly	Gln	Gly	Glu	Leu	Pro
	370					375					380				
Gln	Cys	Phe	Cys	Arg	Met	Cys	Ala	Val	Phe	Gly	Gly	Ile	Tyr	Cys	Leu
385					390					395					400
Arg	His	Ser	Val	Gln	Cys	Leu	Val	Val	Asp	Lys	Glu	Ser	Arg	Lys	Cys
				405					410					415	
Lys	Ala	Ile	Ile	Asp	Gln	Phe	Gly	Gln	Arg	Ile	Ile	Ser	Glu	His	Phe
			420					425					430		
Leu	Val	Glu	Asp	Ser	Tyr	Phe	Pro	Glu	Asn	Met	Cys	Ser	Arg	Val	Gln
		435					440					445			
Tyr	Arg	Gln	Ile	Ser	Arg	Ala	Val	Leu	Ile	Thr	Asp	Arg	Ser	Val	Leu
	450					455					460				
Lys	Thr	Asp	Ser	Asp	Gln	Gln	Ile	Ser	Ile	Leu	Thr	Val	Pro	Ala	Glu
465					470					475					480
Glu	Pro	Gly	Thr	Phe	Ala	Val	Arg	Val	Ile	Glu	Leu	Cys	Ser	Ser	Thr
				485					490					495	
Met	Thr	Cys	Met	Lys	Gly	Thr	Tyr	Leu	Val	His	Leu	Thr	Cys	Thr	Ser
			500					505					510		
Ser	Lys	Thr	Ala	Arg	Glu	Asp	Leu	Glu	Ser	Val	Val	Gln	Lys	Leu	Phe
		515					520					525			
Val	Pro	Tyr	Thr	Glu	Met	Glu	Ile	Glu	Asn	Glu	Gln	Val	Glu	Lys	Pro
	530					535					540				
Arg	Ile	Leu	Trp	Ala	Leu	Tyr	Phe	Asn	Met	Arg	Asp	Ser	Ser	Asp	Ile
545					550					555					560
Ser	Arg	Ser	Cys	Tyr	Asn	Asp	Leu	Pro	Ser	Asn	Val	Tyr	Val	Cys	Ser
				565					570					575	
Gly	Pro	Asp	Cys	Gly	Leu	Gly	Asn	Asp	Asn	Ala	Val	Lys	Gln	Ala	Glu

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580	585	590
Thr Leu Phe Gln Glu Ile Cys Pro Asn Glu Asp Phe Cys Pro Pro Pro		
595	600	605
Pro Asn Pro Glu Asp Ile Ile Leu Asp Gly Asp Ser Leu Gln Pro Glu		
610	615	620
Ala Ser Glu Ser Ser Ala Ile Pro Glu Ala Asn Ser Glu Thr Phe Lys		
625	630	635
Glu Ser Thr Asn Leu Gly Asn Leu Glu Glu Ser Ser Glu		
645	650	

<210> SEQ ID NO 17  
 <211> LENGTH: 212  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17

Met Ala Ser Leu Phe Ser Gly Arg Ile Leu Ile Arg Asn Asn Ser Asp		
1	5	10
Gln Asp Glu Leu Asp Thr Glu Ala Glu Val Ser Arg Arg Leu Glu Asn		
20	25	30
Arg Leu Val Leu Leu Phe Phe Gly Ala Gly Ala Cys Pro Gln Cys Gln		
35	40	45
Ala Phe Val Pro Ile Leu Lys Asp Phe Phe Val Arg Leu Thr Asp Glu		
50	55	60
Phe Tyr Val Leu Arg Ala Ala Gln Leu Ala Leu Val Tyr Val Ser Gln		
65	70	75
Asp Ser Thr Glu Glu Gln Gln Asp Leu Phe Leu Lys Asp Met Pro Lys		
85	90	95
Lys Trp Leu Phe Leu Pro Phe Glu Asp Asp Leu Arg Arg Asp Leu Gly		
100	105	110
Arg Gln Phe Ser Val Glu Arg Leu Pro Ala Val Val Val Leu Lys Pro		
115	120	125
Asp Gly Asp Val Leu Thr Arg Asp Gly Ala Asp Glu Ile Gln Arg Leu		
130	135	140
Gly Thr Ala Cys Phe Ala Asn Trp Gln Glu Ala Ala Glu Val Leu Asp		
145	150	155
Arg Asn Phe Gln Leu Pro Glu Asp Leu Glu Asp Gln Glu Pro Arg Ser		
165	170	175
Leu Thr Glu Cys Leu Arg Arg His Lys Tyr Arg Val Glu Lys Ala Ala		
180	185	190
Arg Gly Gly Arg Asp Pro Gly Gly Gly Gly Gly Glu Glu Gly Gly Ala		
195	200	205
Gly Gly Leu Phe		
210		

<210> SEQ ID NO 18  
 <211> LENGTH: 156  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

Met Val Asp Ile Leu Gly Glu Arg His Leu Val Thr Cys Lys Gly Ala		
1	5	10
Thr Val Glu Ala Glu Ala Ala Leu Gln Asn Lys Val Val Ala Leu Tyr		
20	25	30
Phe Ala Ala Ala Arg Cys Ala Pro Ser Arg Asp Phe Thr Pro Leu Leu		

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35	40	45
Cys Asp Phe Tyr Thr Ala Leu Val Ala Glu Ala Arg Arg Pro Ala Pro 50 55 60		
Phe Glu Val Val Phe Val Ser Ala Asp Gly Ser Ser Gln Glu Met Leu 65 70 75 80		
Asp Phe Met Arg Glu Leu His Gly Ala Trp Leu Ala Leu Pro Phe His 85 90 95		
Asp Pro Tyr Arg His Glu Leu Arg Lys Arg Tyr Asn Val Thr Ala Ile 100 105 110		
Pro Lys Leu Val Ile Val Lys Gln Asn Gly Glu Val Ile Thr Asn Lys 115 120 125		
Gly Arg Lys Gln Ile Arg Glu Arg Gly Leu Ala Cys Phe Gln Asp Trp 130 135 140		
Val Glu Ala Ala Asp Ile Phe Gln Asn Phe Ser Val 145 150 155		

<210> SEQ ID NO 19  
 <211> LENGTH: 135  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

Met Val Asp Ile Leu Gly Glu Arg His Leu Val Thr Cys Lys Gly Ala 1 5 10 15
Thr Val Glu Ala Glu Ala Ala Leu Gln Asn Lys Val Val Ala Leu Tyr 20 25 30
Phe Ala Ala Ala Arg Cys Ala Pro Ser Arg Asp Phe Thr Pro Leu Leu 35 40 45
Cys Asp Phe Tyr Thr Ala Leu Val Ala Glu Ala Arg Arg Pro Ala Pro 50 55 60
Phe Glu Val Val Phe Val Ser Ala Asp Gly Ser Ser Gln Glu Met Leu 65 70 75 80
Asp Phe Met Arg Glu Leu His Gly Ala Trp Leu Ala Leu Pro Phe His 85 90 95
Asp Pro Tyr Arg Gln Arg Ser Leu Ala Leu Leu Pro Arg Leu Glu Cys 100 105 110
Ser Gly Val Ile Leu Ala His Cys Asn Leu Cys Leu Leu Gly Ser Ser 115 120 125
Asp Ser Leu Ala Leu Ala Ser 130 135

<210> SEQ ID NO 20  
 <211> LENGTH: 860  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

Met Gly Glu Val Thr Ala Glu Glu Val Glu Lys Phe Leu Asp Ser Asn 1 5 10 15
Ile Gly Phe Ala Lys Gln Tyr Tyr Asn Leu His Tyr Arg Ala Lys Leu 20 25 30
Ile Ser Asp Leu Leu Gly Ala Lys Glu Ala Ala Val Asp Phe Ser Asn 35 40 45
Tyr His Ser Pro Ser Ser Met Glu Glu Ser Glu Ile Ile Phe Asp Leu 50 55 60
Leu Arg Asp Phe Gln Glu Asn Leu Gln Thr Glu Lys Cys Ile Phe Asn

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65	70	75	80
Val Met Lys Lys Leu Cys Phe Leu Leu Gln Ala Asp Arg Met Ser Leu 85 90 95			
Phe Met Tyr Arg Thr Arg Asn Gly Ile Ala Glu Leu Ala Thr Arg Leu 100 105 110			
Phe Asn Val His Lys Asp Ala Val Leu Glu Asp Cys Leu Val Met Pro 115 120 125			
Asp Gln Glu Ile Val Phe Pro Leu Asp Met Gly Ile Val Gly His Val 130 135 140			
Ala His Ser Lys Lys Ile Ala Asn Val Pro Asn Thr Glu Glu Asp Glu 145 150 155 160			
His Phe Cys Asp Phe Val Asp Ile Leu Thr Glu Tyr Lys Thr Lys Asn 165 170 175			
Ile Leu Ala Ser Pro Ile Met Asn Gly Lys Asp Val Val Ala Ile Ile 180 185 190			
Met Ala Val Asn Lys Val Asp Gly Ser His Phe Thr Lys Arg Asp Glu 195 200 205			
Glu Ile Leu Leu Lys Tyr Leu Asn Phe Ala Asn Leu Ile Met Lys Val 210 215 220			
Tyr His Leu Ser Tyr Leu His Asn Cys Glu Thr Arg Arg Gly Gln Ile 225 230 235 240			
Leu Leu Trp Ser Gly Ser Lys Val Phe Glu Glu Leu Thr Asp Ile Glu 245 250 255			
Arg Gln Phe His Lys Ala Leu Tyr Thr Val Arg Ala Phe Leu Asn Cys 260 265 270			
Asp Arg Tyr Ser Val Gly Leu Leu Asp Met Thr Lys Gln Lys Glu Phe 275 280 285			
Phe Asp Val Trp Pro Val Leu Met Gly Glu Val Pro Pro Tyr Ser Gly 290 295 300			
Pro Arg Thr Pro Asp Gly Arg Glu Ile Asn Phe Tyr Lys Val Ile Asp 305 310 315 320			
Tyr Ile Leu His Gly Lys Glu Asp Ile Lys Val Ile Pro Asn Pro Pro 325 330 335			
Pro Asp His Trp Ala Leu Val Ser Gly Leu Pro Ala Tyr Val Ala Gln 340 345 350			
Asn Gly Leu Ile Cys Asn Ile Met Asn Ala Pro Ala Glu Asp Phe Phe 355 360 365			
Ala Phe Gln Lys Glu Pro Leu Asp Glu Ser Gly Trp Met Ile Lys Asn 370 375 380			
Val Leu Ser Met Pro Ile Val Asn Lys Lys Glu Glu Ile Val Gly Val 385 390 395 400			
Ala Thr Phe Tyr Asn Arg Lys Asp Gly Lys Pro Phe Asp Glu Met Asp 405 410 415			
Glu Thr Leu Met Glu Ser Leu Thr Gln Phe Leu Gly Trp Ser Val Leu 420 425 430			
Asn Pro Asp Thr Tyr Glu Ser Met Asn Lys Leu Glu Asn Arg Lys Asp 435 440 445			
Ile Phe Gln Asp Ile Val Lys Tyr His Val Lys Cys Asp Asn Glu Glu 450 455 460			
Ile Gln Lys Ile Leu Lys Thr Arg Glu Val Tyr Gly Lys Glu Pro Trp 465 470 475 480			
Glu Cys Glu Glu Glu Glu Leu Ala Glu Ile Leu Gln Ala Glu Leu Pro 485 490 495			

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Asp Ala Asp Lys Tyr Glu Ile Asn Lys Phe His Phe Ser Asp Leu Pro  
 500 505 510  
 Leu Thr Glu Leu Glu Leu Val Lys Cys Gly Ile Gln Met Tyr Tyr Glu  
 515 520 525  
 Leu Lys Val Val Asp Lys Phe His Ile Pro Gln Glu Ala Leu Val Arg  
 530 535 540  
 Phe Met Tyr Ser Leu Ser Lys Gly Tyr Arg Lys Ile Thr Tyr His Asn  
 545 550 555 560  
 Trp Arg His Gly Phe Asn Val Gly Gln Thr Met Phe Ser Leu Leu Val  
 565 570 575  
 Thr Gly Lys Leu Lys Arg Tyr Phe Thr Asp Leu Glu Ala Leu Ala Met  
 580 585 590  
 Val Thr Ala Ala Phe Cys His Asp Ile Asp His Arg Gly Thr Asn Asn  
 595 600 605  
 Leu Tyr Gln Met Lys Ser Gln Asn Pro Leu Ala Lys Leu His Gly Ser  
 610 615 620  
 Ser Ile Leu Glu Arg His His Leu Glu Phe Gly Lys Thr Leu Leu Arg  
 625 630 635 640  
 Asp Glu Ser Leu Asn Ile Phe Gln Asn Leu Asn Arg Arg Gln His Glu  
 645 650 655  
 His Ala Ile His Met Met Asp Ile Ala Ile Ile Ala Thr Asp Leu Ala  
 660 665 670  
 Leu Tyr Phe Lys Lys Arg Thr Met Phe Gln Lys Ile Val Asp Gln Ser  
 675 680 685  
 Lys Thr Tyr Glu Ser Glu Gln Glu Trp Thr Gln Tyr Met Met Leu Glu  
 690 695 700  
 Gln Thr Arg Lys Glu Ile Val Met Ala Met Met Met Thr Ala Cys Asp  
 705 710 715 720  
 Leu Ser Ala Ile Thr Lys Pro Trp Glu Val Gln Ser Gln Val Ala Leu  
 725 730 735  
 Leu Val Ala Ala Glu Phe Trp Glu Gln Gly Asp Leu Glu Arg Thr Val  
 740 745 750  
 Leu Gln Gln Asn Pro Ile Pro Met Met Asp Arg Asn Lys Ala Asp Glu  
 755 760 765  
 Leu Pro Lys Leu Gln Val Gly Phe Ile Asp Phe Val Cys Thr Phe Val  
 770 775 780  
 Tyr Lys Glu Phe Ser Arg Phe His Glu Glu Ile Thr Pro Met Leu Asp  
 785 790 795 800  
 Gly Ile Thr Asn Asn Arg Lys Glu Trp Lys Ala Leu Ala Asp Glu Tyr  
 805 810 815  
 Asp Ala Lys Met Lys Val Gln Glu Glu Lys Lys Gln Lys Gln Gln Ser  
 820 825 830  
 Ala Lys Ser Ala Ala Ala Gly Asn Gln Pro Gly Gly Asn Pro Ser Pro  
 835 840 845  
 Gly Gly Ala Thr Thr Ser Lys Ser Cys Cys Ile Gln  
 850 855 860

&lt;210&gt; SEQ ID NO 21

&lt;211&gt; LENGTH: 854

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 21

Met Ser Leu Ser Glu Glu Gln Ala Arg Ser Phe Leu Asp Gln Asn Pro

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1	5	10	15
Asp Phe Ala Arg Gln Tyr Phe Gly Lys Lys Leu Ser Pro Glu Asn Val	20	25	30
Ala Ala Ala Cys Glu Asp Gly Cys Pro Pro Asp Cys Asp Ser Leu Arg	35	40	45
Asp Leu Cys Gln Val Glu Glu Ser Thr Ala Leu Leu Glu Leu Val Gln	50	55	60
Asp Met Gln Glu Ser Ile Asn Met Glu Arg Val Val Phe Lys Val Leu	65	70	75
Arg Arg Leu Cys Thr Leu Leu Gln Ala Asp Arg Cys Ser Leu Phe Met	85	90	95
Tyr Arg Gln Arg Asn Gly Val Ala Glu Leu Ala Thr Arg Leu Phe Ser	100	105	110
Val Gln Pro Asp Ser Val Leu Glu Asp Cys Leu Val Pro Pro Asp Ser	115	120	125
Glu Ile Val Phe Pro Leu Asp Ile Gly Val Val Gly His Val Ala Gln	130	135	140
Thr Lys Lys Met Val Asn Val Glu Asp Val Ala Glu Cys Pro His Phe	145	150	155
Ser Ser Phe Ala Asp Glu Leu Thr Asp Tyr Lys Thr Lys Asn Met Leu	165	170	175
Ala Thr Pro Ile Met Asn Gly Lys Asp Val Val Ala Val Ile Met Ala	180	185	190
Val Asn Lys Leu Asn Gly Pro Phe Phe Thr Ser Glu Asp Glu Asp Val	195	200	205
Phe Leu Lys Tyr Leu Asn Phe Ala Thr Leu Tyr Leu Lys Ile Tyr His	210	215	220
Leu Ser Tyr Leu His Asn Cys Glu Thr Arg Arg Gly Gln Val Leu Leu	225	230	235
Trp Ser Ala Asn Lys Val Phe Glu Glu Leu Thr Asp Ile Glu Arg Gln	245	250	255
Phe His Lys Ala Phe Tyr Thr Val Arg Ala Tyr Leu Asn Cys Glu Arg	260	265	270
Tyr Ser Val Gly Leu Leu Asp Met Thr Lys Glu Lys Glu Phe Phe Asp	275	280	285
Val Trp Ser Val Leu Met Gly Glu Ser Gln Pro Tyr Ser Gly Pro Arg	290	295	300
Thr Pro Asp Gly Arg Glu Ile Val Phe Tyr Lys Val Ile Asp Tyr Ile	305	310	315
Leu His Gly Lys Glu Glu Ile Lys Val Ile Pro Thr Pro Ser Ala Asp	325	330	335
His Trp Ala Leu Ala Ser Gly Leu Pro Ser Tyr Val Ala Glu Ser Gly	340	345	350
Phe Ile Cys Asn Ile Met Asn Ala Ser Ala Asp Glu Met Phe Lys Phe	355	360	365
Gln Glu Gly Ala Leu Asp Asp Ser Gly Trp Leu Ile Lys Asn Val Leu	370	375	380
Ser Met Pro Ile Val Asn Lys Lys Glu Glu Ile Val Gly Val Ala Thr	385	390	395
Phe Tyr Asn Arg Lys Asp Gly Lys Pro Phe Asp Glu Gln Asp Glu Val	405	410	415
Leu Met Glu Ser Leu Thr Gln Phe Leu Gly Trp Ser Val Met Asn Thr	420	425	430



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Asp Thr Tyr Asp Lys Met Asn Lys Leu Glu Asn Arg Lys Asp Ile Ala  
 435 440 445

Gln Asp Met Val Leu Tyr His Val Lys Cys Asp Arg Asp Glu Ile Gln  
 450 455 460

Leu Ile Leu Pro Thr Arg Ala Arg Leu Gly Lys Glu Pro Ala Asp Cys  
 465 470 475 480

Asp Glu Asp Glu Leu Gly Glu Ile Leu Lys Glu Glu Leu Pro Gly Pro  
 485 490 495

Thr Thr Phe Asp Ile Tyr Glu Phe His Phe Ser Asp Leu Glu Cys Thr  
 500 505 510

Glu Leu Asp Leu Val Lys Cys Gly Ile Gln Met Tyr Tyr Glu Leu Gly  
 515 520 525

Val Val Arg Lys Phe Gln Ile Pro Gln Glu Val Leu Val Arg Phe Leu  
 530 535 540

Phe Ser Ile Ser Lys Gly Tyr Arg Arg Ile Thr Tyr His Asn Trp Arg  
 545 550 555 560

His Gly Phe Asn Val Ala Gln Thr Met Phe Thr Leu Leu Met Thr Gly  
 565 570 575

Lys Leu Lys Ser Tyr Tyr Thr Asp Leu Glu Ala Phe Ala Met Val Thr  
 580 585 590

Ala Gly Leu Cys His Asp Ile Asp His Arg Gly Thr Asn Asn Leu Tyr  
 595 600 605

Gln Met Lys Ser Gln Asn Pro Leu Ala Lys Leu His Gly Ser Ser Ile  
 610 615 620

Leu Glu Arg His His Leu Glu Phe Gly Lys Phe Leu Leu Ser Glu Glu  
 625 630 635 640

Thr Leu Asn Ile Tyr Gln Asn Leu Asn Arg Arg Gln His Glu His Val  
 645 650 655

Ile His Leu Met Asp Ile Ala Ile Ile Ala Thr Asp Leu Ala Leu Tyr  
 660 665 670

Phe Lys Lys Arg Ala Met Phe Gln Lys Ile Val Asp Glu Ser Lys Asn  
 675 680 685

Tyr Gln Asp Lys Lys Ser Trp Val Glu Tyr Leu Ser Leu Glu Thr Thr  
 690 695 700

Arg Lys Glu Ile Val Met Ala Met Met Met Thr Ala Cys Asp Leu Ser  
 705 710 715 720

Ala Ile Thr Lys Pro Trp Glu Val Gln Ser Lys Val Ala Leu Leu Val  
 725 730 735

Ala Ala Glu Phe Trp Glu Gln Gly Asp Leu Glu Arg Thr Val Leu Asp  
 740 745 750

Gln Gln Pro Ile Pro Met Met Asp Arg Asn Lys Ala Ala Glu Leu Pro  
 755 760 765

Lys Leu Gln Val Gly Phe Ile Asp Phe Val Cys Thr Phe Val Tyr Lys  
 770 775 780

Glu Phe Ser Arg Phe His Glu Glu Ile Leu Pro Met Phe Asp Arg Leu  
 785 790 795 800

Gln Asn Asn Arg Lys Glu Trp Lys Ala Leu Ala Asp Glu Tyr Glu Ala  
 805 810 815

Lys Val Lys Ala Leu Glu Glu Lys Glu Glu Glu Glu Arg Val Ala Ala  
 820 825 830

Lys Lys Val Gly Thr Glu Ile Cys Asn Gly Gly Pro Ala Pro Lys Ser  
 835 840 845

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Ser Thr Cys Cys Ile Leu  
850

<210> SEQ ID NO 22

<211> LENGTH: 853

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

Met Ser Leu Ser Glu Glu Gln Ala Arg Ser Phe Leu Asp Gln Asn Pro  
1 5 10 15

Asp Phe Ala Arg Gln Tyr Phe Gly Lys Lys Leu Ser Pro Glu Asn Val  
20 25 30

Ala Ala Ala Cys Glu Asp Gly Cys Pro Pro Asp Cys Asp Ser Leu Arg  
35 40 45

Asp Leu Cys Gln Val Glu Glu Ser Thr Ala Leu Leu Glu Leu Val Gln  
50 55 60

Asp Met Gln Glu Ser Ile Asn Met Glu Arg Val Val Phe Lys Val Leu  
65 70 75 80

Arg Arg Leu Cys Thr Leu Leu Gln Ala Asp Arg Cys Ser Leu Phe Met  
85 90 95

Tyr Arg Gln Arg Asn Gly Val Ala Glu Leu Ala Thr Arg Leu Phe Ser  
100 105 110

Val Gln Pro Asp Ser Val Leu Glu Asp Cys Leu Val Pro Pro Asp Ser  
115 120 125

Glu Ile Val Phe Pro Leu Asp Ile Gly Val Val Gly His Val Ala Gln  
130 135 140

Thr Lys Lys Met Val Asn Val Glu Asp Val Ala Glu Cys Pro His Phe  
145 150 155 160

Ser Ser Phe Ala Asp Glu Leu Thr Asp Tyr Lys Thr Lys Asn Met Leu  
165 170 175

Ala Thr Pro Ile Met Asn Gly Lys Asp Val Val Ala Val Ile Met Ala  
180 185 190

Val Asn Lys Leu Asn Gly Pro Phe Phe Thr Ser Glu Asp Glu Asp Val  
195 200 205

Phe Leu Lys Tyr Leu Asn Phe Ala Thr Leu Tyr Leu Lys Ile Tyr His  
210 215 220

Leu Ser Tyr Leu His Asn Cys Glu Thr Arg Arg Gly Gln Val Leu Leu  
225 230 235 240

Trp Ser Ala Asn Lys Val Phe Glu Glu Leu Thr Asp Ile Glu Arg Gln  
245 250 255

Phe His Lys Ala Phe Tyr Thr Val Arg Ala Tyr Leu Asn Cys Glu Arg  
260 265 270

Tyr Ser Val Gly Leu Leu Asp Met Thr Lys Glu Lys Glu Phe Phe Asp  
275 280 285

Val Trp Ser Val Leu Met Gly Glu Ser Gln Pro Tyr Ser Gly Pro Arg  
290 295 300

Thr Pro Asp Gly Arg Glu Ile Val Phe Tyr Lys Val Ile Asp Tyr Ile  
305 310 315 320

Leu His Gly Lys Glu Glu Ile Lys Val Ile Pro Thr Pro Ser Ala Asp  
325 330 335

His Trp Ala Leu Ala Ser Gly Leu Pro Ser Tyr Val Ala Glu Ser Gly  
340 345 350

Phe Ile Cys Asn Ile Met Asn Ala Ser Ala Asp Glu Met Phe Lys Phe  
355 360 365

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Gln Glu Gly Ala Leu Asp Asp Ser Gly Trp Leu Ile Lys Asn Val Leu  
 370 375 380

Ser Met Pro Ile Val Asn Lys Lys Glu Glu Ile Val Gly Val Ala Thr  
 385 390 395 400

Phe Tyr Asn Arg Lys Asp Gly Lys Pro Phe Asp Glu Gln Asp Glu Val  
 405 410 415

Leu Met Glu Ser Leu Thr Gln Phe Leu Gly Trp Ser Val Met Asn Thr  
 420 425 430

Asp Thr Tyr Asp Lys Met Asn Lys Leu Glu Asn Arg Lys Asp Ile Ala  
 435 440 445

Gln Asp Met Val Leu Tyr His Val Lys Cys Asp Arg Asp Glu Ile Gln  
 450 455 460

Leu Ile Leu Pro Thr Arg Ala Arg Leu Gly Lys Glu Pro Ala Asp Cys  
 465 470 475 480

Asp Glu Asp Glu Leu Gly Glu Ile Leu Lys Glu Glu Leu Pro Gly Pro  
 485 490 495

Thr Thr Phe Asp Ile Tyr Glu Phe His Phe Ser Asp Leu Glu Cys Thr  
 500 505 510

Glu Leu Asp Leu Val Lys Cys Gly Ile Gln Met Tyr Tyr Glu Leu Gly  
 515 520 525

Val Val Arg Lys Phe Gln Ile Pro Gln Glu Val Leu Val Arg Phe Leu  
 530 535 540

Phe Ser Ile Ser Lys Gly Tyr Arg Arg Ile Thr Tyr His Asn Trp Arg  
 545 550 555 560

His Gly Phe Asn Val Ala Gln Thr Met Phe Thr Leu Leu Met Thr Gly  
 565 570 575

Lys Leu Lys Ser Tyr Tyr Thr Asp Leu Glu Ala Phe Ala Met Val Thr  
 580 585 590

Ala Gly Leu Cys His Asp Ile Asp His Arg Gly Thr Asn Asn Leu Tyr  
 595 600 605

Gln Met Lys Ser Gln Asn Pro Leu Ala Lys Leu His Gly Ser Ser Ile  
 610 615 620

Leu Glu Arg His His Leu Glu Phe Gly Lys Phe Leu Leu Ser Glu Glu  
 625 630 635 640

Thr Leu Asn Ile Tyr Gln Asn Leu Asn Arg Arg Gln His Glu His Val  
 645 650 655

Ile His Leu Met Asp Ile Ala Ile Ile Ala Thr Asp Leu Ala Leu Tyr  
 660 665 670

Phe Lys Lys Arg Ala Met Phe Gln Lys Ile Val Asp Glu Ser Lys Asn  
 675 680 685

Tyr Gln Asp Lys Lys Ser Trp Val Glu Tyr Leu Ser Leu Glu Thr Thr  
 690 695 700

Arg Lys Glu Ile Val Met Ala Met Met Met Thr Ala Cys Asp Leu Ser  
 705 710 715 720

Ala Ile Thr Lys Pro Trp Glu Val Gln Ser Lys Val Ala Leu Leu Val  
 725 730 735

Ala Ala Glu Phe Trp Glu Gln Gly Asp Leu Glu Arg Thr Val Leu Asp  
 740 745 750

Gln Gln Pro Ile Pro Met Met Asp Arg Asn Lys Ala Ala Glu Leu Pro  
 755 760 765

Lys Leu Gln Val Gly Phe Ile Asp Phe Val Cys Thr Phe Val Tyr Lys  
 770 775 780

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Glu Phe Ser Arg Phe His Glu Glu Ile Leu Pro Met Phe Asp Arg Leu  
785 790 795 800

Gln Asn Asn Arg Lys Glu Trp Lys Ala Leu Ala Asp Glu Tyr Glu Ala  
805 810 815

Lys Val Lys Ala Leu Glu Glu Lys Glu Glu Glu Glu Arg Val Ala Ala  
820 825 830

Lys Lys Gly Thr Glu Ile Cys Asn Gly Gly Pro Ala Pro Lys Ser Ser  
835 840 845

Thr Cys Cys Ile Leu  
850

<210> SEQ ID NO 23  
<211> LENGTH: 575  
<212> TYPE: PRT  
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 23

Met Thr Lys Glu Lys Glu Phe Phe Asp Val Trp Ser Val Leu Met Gly  
1 5 10 15

Glu Ser Gln Pro Tyr Ser Gly Pro Arg Thr Pro Asp Gly Arg Glu Ile  
20 25 30

Val Phe Tyr Lys Val Ile Asp Tyr Ile Leu His Gly Lys Glu Glu Ile  
35 40 45

Lys Val Ile Pro Thr Pro Ser Ala Asp His Trp Ala Leu Ala Ser Gly  
50 55 60

Leu Pro Ser Tyr Val Ala Glu Ser Gly Phe Ile Cys Asn Ile Met Asn  
65 70 75 80

Ala Ser Ala Asp Glu Met Phe Lys Phe Gln Glu Gly Ala Leu Asp Asp  
85 90 95

Ser Gly Trp Leu Ile Lys Asn Val Leu Ser Met Pro Ile Val Asn Lys  
100 105 110

Lys Glu Glu Ile Val Gly Val Ala Thr Phe Tyr Asn Arg Lys Asp Gly  
115 120 125

Lys Pro Phe Asp Glu Gln Asp Glu Val Leu Met Glu Ser Leu Thr Gln  
130 135 140

Phe Leu Gly Trp Ser Val Met Asn Thr Asp Thr Tyr Asp Lys Met Asn  
145 150 155 160

Lys Leu Glu Asn Arg Lys Asp Ile Ala Gln Asp Met Val Leu Tyr His  
165 170 175

Val Lys Cys Asp Arg Asp Glu Ile Gln Leu Ile Leu Pro Thr Arg Ala  
180 185 190

Arg Leu Gly Lys Glu Pro Ala Asp Cys Asp Glu Asp Glu Leu Gly Glu  
195 200 205

Ile Leu Lys Glu Glu Leu Pro Gly Pro Thr Thr Phe Asp Ile Tyr Glu  
210 215 220

Phe His Phe Ser Asp Leu Glu Cys Thr Glu Leu Asp Leu Val Lys Cys  
225 230 235 240

Gly Ile Gln Met Tyr Tyr Glu Leu Gly Val Val Arg Lys Phe Gln Ile  
245 250 255

Pro Gln Glu Val Leu Val Arg Phe Leu Phe Ser Ile Ser Lys Gly Tyr  
260 265 270

Arg Arg Ile Thr Tyr His Asn Trp Arg His Gly Phe Asn Val Ala Gln  
275 280 285

Thr Met Phe Thr Leu Leu Met Thr Gly Lys Leu Lys Ser Tyr Tyr Thr  
290 295 300

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Asp Leu Glu Ala Phe Ala Met Val Thr Ala Gly Leu Cys His Asp Ile  
 305 310 315 320  
 Asp His Arg Gly Thr Asn Asn Leu Tyr Gln Met Lys Ser Gln Asn Pro  
 325 330 335  
 Leu Ala Lys Leu His Gly Ser Ser Ile Leu Glu Arg His His Leu Glu  
 340 345 350  
 Phe Gly Lys Phe Leu Leu Ser Glu Glu Thr Leu Asn Ile Tyr Gln Asn  
 355 360 365  
 Leu Asn Arg Arg Gln His Glu His Val Ile His Leu Met Asp Ile Ala  
 370 375 380  
 Ile Ile Ala Thr Asp Leu Ala Leu Tyr Phe Lys Lys Arg Ala Met Phe  
 385 390 395 400  
 Gln Lys Ile Val Asp Glu Ser Lys Asn Tyr Gln Asp Lys Lys Ser Trp  
 405 410 415  
 Val Glu Tyr Leu Ser Leu Glu Thr Thr Arg Lys Glu Ile Val Met Ala  
 420 425 430  
 Met Met Met Thr Ala Cys Asp Leu Ser Ala Ile Thr Lys Pro Trp Glu  
 435 440 445  
 Val Gln Ser Lys Val Ala Leu Leu Val Ala Ala Glu Phe Trp Glu Gln  
 450 455 460  
 Gly Asp Leu Glu Arg Thr Val Leu Asp Gln Gln Pro Ile Pro Met Met  
 465 470 475 480  
 Asp Arg Asn Lys Ala Ala Glu Leu Pro Lys Leu Gln Val Gly Phe Ile  
 485 490 495  
 Asp Phe Val Cys Thr Phe Val Tyr Lys Glu Phe Ser Arg Phe His Glu  
 500 505 510  
 Glu Ile Leu Pro Met Phe Asp Arg Leu Gln Asn Asn Arg Lys Glu Trp  
 515 520 525  
 Lys Ala Leu Ala Asp Glu Tyr Glu Ala Lys Val Lys Ala Leu Glu Glu  
 530 535 540  
 Lys Glu Glu Glu Glu Arg Val Ala Ala Lys Lys Val Gly Thr Glu Ile  
 545 550 555 560  
 Cys Asn Gly Gly Pro Ala Pro Lys Ser Ser Thr Cys Cys Ile Leu  
 565 570 575

&lt;210&gt; SEQ ID NO 24

&lt;211&gt; LENGTH: 694

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 24

Met Ala Lys Ile Asn Thr Gln Tyr Ser His Pro Ser Arg Thr His Leu  
 1 5 10 15  
 Lys Val Lys Thr Ser Asp Arg Asp Leu Asn Arg Ala Glu Asn Gly Leu  
 20 25 30  
 Ser Arg Ala His Ser Ser Ser Glu Glu Thr Ser Ser Val Leu Gln Pro  
 35 40 45  
 Gly Ile Ala Met Glu Thr Arg Gly Leu Ala Asp Ser Gly Gln Gly Ser  
 50 55 60  
 Phe Thr Gly Gln Gly Ile Ala Arg Leu Ser Arg Leu Ile Phe Leu Leu  
 65 70 75 80  
 Arg Arg Trp Ala Ala Arg His Val His His Gln Asp Gln Gly Pro Asp  
 85 90 95  
 Ser Phe Pro Asp Arg Phe Arg Gly Ala Glu Leu Lys Glu Val Ser Ser

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100					105					110					
Gln	Glu	Ser	Asn	Ala	Gln	Ala	Asn	Val	Gly	Ser	Gln	Glu	Pro	Ala	Asp
		115					120					125			
Arg	Gly	Arg	Ser	Ala	Trp	Pro	Leu	Ala	Lys	Cys	Asn	Thr	Asn	Thr	Ser
	130					135					140				
Asn	Asn	Thr	Glu	Glu	Glu	Lys	Lys	Thr	Lys	Lys	Lys	Asp	Ala	Ile	Val
145						150					155				160
Val	Asp	Pro	Ser	Ser	Asn	Leu	Tyr	Tyr	Arg	Trp	Leu	Thr	Ala	Ile	Ala
				165					170					175	
Leu	Pro	Val	Phe	Tyr	Asn	Trp	Tyr	Leu	Leu	Ile	Cys	Arg	Ala	Cys	Phe
			180					185					190		
Asp	Glu	Leu	Gln	Ser	Glu	Tyr	Leu	Met	Leu	Trp	Leu	Val	Leu	Asp	Tyr
		195					200					205			
Ser	Ala	Asp	Val	Leu	Tyr	Val	Leu	Asp	Val	Leu	Val	Arg	Ala	Arg	Thr
	210					215					220				
Gly	Phe	Leu	Glu	Gln	Gly	Leu	Met	Val	Ser	Asp	Thr	Asn	Arg	Leu	Trp
225						230					235				240
Gln	His	Tyr	Lys	Thr	Thr	Thr	Gln	Phe	Lys	Leu	Asp	Val	Leu	Ser	Leu
				245					250					255	
Val	Pro	Thr	Asp	Leu	Ala	Tyr	Leu	Lys	Val	Gly	Thr	Asn	Tyr	Pro	Glu
			260					265					270		
Val	Arg	Phe	Asn	Arg	Leu	Leu	Lys	Phe	Ser	Arg	Leu	Phe	Glu	Phe	Phe
		275					280					285			
Asp	Arg	Thr	Glu	Thr	Arg	Thr	Asn	Tyr	Pro	Asn	Met	Phe	Arg	Ile	Gly
	290					295					300				
Asn	Leu	Val	Leu	Tyr	Ile	Leu	Ile	Ile	Ile	His	Trp	Asn	Ala	Cys	Ile
305						310					315				320
Tyr	Phe	Ala	Ile	Ser	Lys	Phe	Ile	Gly	Phe	Gly	Thr	Asp	Ser	Trp	Val
				325					330					335	
Tyr	Pro	Asn	Ile	Ser	Ile	Pro	Glu	His	Gly	Arg	Leu	Ser	Arg	Lys	Tyr
			340					345					350		
Ile	Tyr	Ser	Leu	Tyr	Trp	Ser	Thr	Leu	Thr	Leu	Thr	Thr	Ile	Gly	Glu
		355					360					365			
Thr	Pro	Pro	Pro	Val	Lys	Asp	Glu	Glu	Tyr	Leu	Phe	Val	Val	Val	Asp
	370					375					380				
Phe	Leu	Val	Gly	Val	Leu	Ile	Phe	Ala	Thr	Ile	Val	Gly	Asn	Val	Gly
385						390					395				400
Ser	Met	Ile	Ser	Asn	Met	Asn	Ala	Ser	Arg	Ala	Glu	Phe	Gln	Ala	Lys
				405					410					415	
Ile	Asp	Ser	Ile	Lys	Gln	Tyr	Met	Gln	Phe	Arg	Lys	Val	Thr	Lys	Asp
			420					425					430		
Leu	Glu	Thr	Arg	Val	Ile	Arg	Trp	Phe	Asp	Tyr	Leu	Trp	Ala	Asn	Lys
		435					440					445			
Lys	Thr	Val	Asp	Glu	Lys	Glu	Val	Leu	Lys	Ser	Leu	Pro	Asp	Lys	Leu
	450					455					460				
Lys	Ala	Glu	Ile	Ala	Ile	Asn	Val	His	Leu	Asp	Thr	Leu	Lys	Lys	Val
465						470					475				480
Arg	Ile	Phe	Gln	Asp	Cys	Glu	Ala	Gly	Leu	Leu	Val	Glu	Leu	Val	Leu
				485					490					495	
Lys	Leu	Arg	Pro	Thr	Val	Phe	Ser	Pro	Gly	Asp	Tyr	Ile	Cys	Lys	Lys
			500					505					510		
Gly	Asp	Ile	Gly	Lys	Glu	Met	Tyr	Ile	Ile	Asn	Glu	Gly	Lys	Leu	Ala
		515					520					525			

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Val Val Ala Asp Asp Gly Val Thr Gln Phe Val Val Leu Ser Asp Gly  
 530 535 540

Ser Tyr Phe Gly Glu Ile Ser Ile Leu Asn Ile Lys Gly Ser Lys Ser  
 545 550 555 560

Gly Asn Arg Arg Thr Ala Asn Ile Arg Ser Ile Gly Tyr Ser Asp Leu  
 565 570 575

Phe Cys Leu Ser Lys Asp Asp Leu Met Glu Ala Leu Thr Glu Tyr Pro  
 580 585 590

Glu Ala Lys Lys Ala Leu Glu Glu Lys Gly Arg Gln Ile Leu Met Lys  
 595 600 605

Asp Asn Leu Ile Asp Glu Glu Leu Ala Arg Ala Gly Ala Asp Pro Lys  
 610 615 620

Asp Leu Glu Glu Lys Val Glu Gln Leu Gly Ser Ser Leu Asp Thr Leu  
 625 630 635 640

Gln Thr Arg Phe Ala Arg Leu Leu Ala Glu Tyr Asn Ala Thr Gln Met  
 645 650 655

Lys Met Lys Gln Arg Leu Ser Gln Leu Glu Ser Gln Val Lys Gly Gly  
 660 665 670

Gly Asp Lys Pro Leu Ala Asp Gly Glu Val Pro Gly Asp Ala Thr Lys  
 675 680 685

Thr Glu Asp Lys Gln Gln  
 690

&lt;210&gt; SEQ ID NO 25

&lt;211&gt; LENGTH: 676

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 25

Met Ala Lys Ile Asn Thr Gln Tyr Ser His Pro Ser Arg Thr His Leu  
 1 5 10 15

Lys Val Lys Thr Ser Asp Arg Asp Leu Asn Arg Ala Glu Asn Gly Leu  
 20 25 30

Ser Arg Ala His Ser Ser Ser Glu Glu Thr Ser Ser Val Leu Gln Pro  
 35 40 45

Gly Ile Ala Met Glu Thr Arg Gly Leu Ala Asp Ser Gly Gln Gly Ser  
 50 55 60

Phe Thr Gly Gln Gly Ile Ala Arg Leu Ser Arg Leu Ile Phe Leu Leu  
 65 70 75 80

Arg Arg Trp Ala Ala Arg His Val His His Gln Asp Gln Gly Pro Asp  
 85 90 95

Ser Phe Pro Asp Arg Phe Arg Gly Ala Glu Leu Lys Glu Val Ser Ser  
 100 105 110

Gln Glu Ser Asn Ala Gln Ala Asn Val Gly Ser Gln Glu Pro Ala Asp  
 115 120 125

Arg Gly Arg Arg Lys Lys Thr Lys Lys Lys Asp Ala Ile Val Val Asp  
 130 135 140

Pro Ser Ser Asn Leu Tyr Tyr Arg Trp Leu Thr Ala Ile Ala Leu Pro  
 145 150 155 160

Val Phe Tyr Asn Trp Tyr Leu Leu Ile Cys Arg Ala Cys Phe Asp Glu  
 165 170 175

Leu Gln Ser Glu Tyr Leu Met Leu Trp Leu Val Leu Asp Tyr Ser Ala  
 180 185 190

Asp Val Leu Tyr Val Leu Asp Val Leu Val Arg Ala Arg Thr Gly Phe

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195				200				205							
Leu	Glu	Gln	Gly	Leu	Met	Val	Ser	Asp	Thr	Asn	Arg	Leu	Trp	Gln	His
	210					215					220				
Tyr	Lys	Thr	Thr	Thr	Gln	Phe	Lys	Leu	Asp	Val	Leu	Ser	Leu	Val	Pro
	225				230					235					240
Thr	Asp	Leu	Ala	Tyr	Leu	Lys	Val	Gly	Thr	Asn	Tyr	Pro	Glu	Val	Arg
				245					250					255	
Phe	Asn	Arg	Leu	Leu	Lys	Phe	Ser	Arg	Leu	Phe	Glu	Phe	Phe	Asp	Arg
			260					265						270	
Thr	Glu	Thr	Arg	Thr	Asn	Tyr	Pro	Asn	Met	Phe	Arg	Ile	Gly	Asn	Leu
		275					280							285	
Val	Leu	Tyr	Ile	Leu	Ile	Ile	Ile	His	Trp	Asn	Ala	Cys	Ile	Tyr	Phe
	290					295					300				
Ala	Ile	Ser	Lys	Phe	Ile	Gly	Phe	Gly	Thr	Asp	Ser	Trp	Val	Tyr	Pro
	305				310					315					320
Asn	Ile	Ser	Ile	Pro	Glu	His	Gly	Arg	Leu	Ser	Arg	Lys	Tyr	Ile	Tyr
				325					330					335	
Ser	Leu	Tyr	Trp	Ser	Thr	Leu	Thr	Leu	Thr	Thr	Ile	Gly	Glu	Thr	Pro
			340						345				350		
Pro	Pro	Val	Lys	Asp	Glu	Glu	Tyr	Leu	Phe	Val	Val	Val	Asp	Phe	Leu
		355					360						365		
Val	Gly	Val	Leu	Ile	Phe	Ala	Thr	Ile	Val	Gly	Asn	Val	Gly	Ser	Met
	370					375					380				
Ile	Ser	Asn	Met	Asn	Ala	Ser	Arg	Ala	Glu	Phe	Gln	Ala	Lys	Ile	Asp
				385		390				395					400
Ser	Ile	Lys	Gln	Tyr	Met	Gln	Phe	Arg	Lys	Val	Thr	Lys	Asp	Leu	Glu
				405					410					415	
Thr	Arg	Val	Ile	Arg	Trp	Phe	Asp	Tyr	Leu	Trp	Ala	Asn	Lys	Lys	Thr
			420					425						430	
Val	Asp	Glu	Lys	Glu	Val	Leu	Lys	Ser	Leu	Pro	Asp	Lys	Leu	Lys	Ala
		435					440						445		
Glu	Ile	Ala	Ile	Asn	Val	His	Leu	Asp	Thr	Leu	Lys	Lys	Val	Arg	Ile
				450		455					460				
Phe	Gln	Asp	Cys	Glu	Ala	Gly	Leu	Leu	Val	Glu	Leu	Val	Leu	Lys	Leu
				465		470				475					480
Arg	Pro	Thr	Val	Phe	Ser	Pro	Gly	Asp	Tyr	Ile	Cys	Lys	Lys	Gly	Asp
				485					490					495	
Ile	Gly	Lys	Glu	Met	Tyr	Ile	Ile	Asn	Glu	Gly	Lys	Leu	Ala	Val	Val
				500				505					510		
Ala	Asp	Asp	Gly	Val	Thr	Gln	Phe	Val	Val	Leu	Ser	Asp	Gly	Ser	Tyr
		515					520						525		
Phe	Gly	Glu	Ile	Ser	Ile	Leu	Asn	Ile	Lys	Gly	Ser	Lys	Ser	Gly	Asn
		530				535				540					
Arg	Arg	Thr	Ala	Asn	Ile	Arg	Ser	Ile	Gly	Tyr	Ser	Asp	Leu	Phe	Cys
				545		550				555					560
Leu	Ser	Lys	Asp	Asp	Leu	Met	Glu	Ala	Leu	Thr	Glu	Tyr	Pro	Glu	Ala
				565					570					575	
Lys	Lys	Ala	Leu	Glu	Glu	Lys	Gly	Arg	Gln	Ile	Leu	Met	Lys	Asp	Asn
			580						585					590	
Leu	Ile	Asp	Glu	Glu	Leu	Ala	Arg	Ala	Gly	Ala	Asp	Pro	Lys	Asp	Leu
		595					600						605		
Glu	Glu	Lys	Val	Glu	Gln	Leu	Gly	Ser	Ser	Leu	Asp	Thr	Leu	Gln	Thr
				610		615					620				



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Arg Phe Ala Arg Leu Leu Ala Glu Tyr Asn Ala Thr Gln Met Lys Met  
625 630 635 640

Lys Gln Arg Leu Ser Gln Leu Glu Ser Gln Val Lys Gly Gly Gly Asp  
645 650 655

Lys Pro Leu Ala Asp Gly Glu Val Pro Gly Asp Ala Thr Lys Thr Glu  
660 665 670

Asp Lys Gln Gln  
675

<210> SEQ ID NO 26  
<211> LENGTH: 809  
<212> TYPE: PRT  
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 26

Met Phe Lys Ser Leu Thr Lys Val Asn Lys Val Lys Pro Ile Gly Glu  
1 5 10 15

Asn Asn Glu Asn Glu Gln Ser Ser Arg Arg Asn Glu Glu Gly Ser His  
20 25 30

Pro Ser Asn Gln Ser Gln Gln Thr Thr Ala Gln Glu Glu Asn Lys Gly  
35 40 45

Glu Glu Lys Ser Leu Lys Thr Lys Ser Thr Pro Val Thr Ser Glu Glu  
50 55 60

Pro His Thr Asn Ile Gln Asp Lys Leu Ser Lys Lys Asn Ser Ser Gly  
65 70 75 80

Asp Leu Thr Thr Asn Pro Asp Pro Gln Asn Ala Ala Glu Pro Thr Gly  
85 90 95

Thr Val Pro Glu Gln Lys Glu Met Asp Pro Gly Lys Glu Gly Pro Asn  
100 105 110

Ser Pro Gln Asn Lys Pro Pro Ala Ala Pro Val Ile Asn Glu Tyr Ala  
115 120 125

Asp Ala Gln Leu His Asn Leu Val Lys Arg Met Arg Gln Arg Thr Ala  
130 135 140

Leu Tyr Lys Lys Lys Leu Val Glu Gly Asp Leu Ser Ser Pro Glu Ala  
145 150 155 160

Ser Pro Gln Thr Ala Lys Pro Thr Ala Val Pro Pro Val Lys Glu Ser  
165 170 175

Asp Asp Lys Pro Thr Glu His Tyr Tyr Arg Leu Leu Trp Phe Lys Val  
180 185 190

Lys Lys Met Pro Leu Thr Glu Tyr Leu Lys Arg Ile Lys Leu Pro Asn  
195 200 205

Ser Ile Asp Ser Tyr Thr Asp Arg Leu Tyr Leu Leu Trp Leu Leu Leu  
210 215 220

Val Thr Leu Ala Tyr Asn Trp Asn Cys Cys Phe Ile Pro Leu Arg Leu  
225 230 235 240

Val Phe Pro Tyr Gln Thr Ala Asp Asn Ile His Tyr Trp Leu Ile Ala  
245 250 255

Asp Ile Ile Cys Asp Ile Ile Tyr Leu Tyr Asp Met Leu Phe Ile Gln  
260 265 270

Pro Arg Leu Gln Phe Val Arg Gly Gly Asp Ile Ile Val Asp Ser Asn  
275 280 285

Glu Leu Arg Lys His Tyr Arg Thr Ser Thr Lys Phe Gln Leu Asp Val  
290 295 300

Ala Ser Ile Ile Pro Phe Asp Ile Cys Tyr Leu Phe Phe Gly Phe Asn

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305	310	315	320
Pro Met Phe Arg Ala Asn Arg Met Leu Lys Tyr Thr Ser Phe Phe Glu 325 330 335			
Phe Asn His His Leu Glu Ser Ile Met Asp Lys Ala Tyr Ile Tyr Arg 340 345 350			
Val Ile Arg Thr Thr Gly Tyr Leu Leu Phe Ile Leu His Ile Asn Ala 355 360 365			
Cys Val Tyr Tyr Trp Ala Ser Asn Tyr Glu Gly Ile Gly Thr Thr Arg 370 375 380			
Trp Val Tyr Asp Gly Glu Gly Asn Glu Tyr Leu Arg Cys Tyr Tyr Trp 385 390 395 400			
Ala Val Arg Thr Leu Ile Thr Ile Gly Gly Leu Pro Glu Pro Gln Thr 405 410 415			
Leu Phe Glu Ile Val Phe Gln Leu Leu Asn Phe Phe Ser Gly Val Phe 420 425 430			
Val Phe Ser Ser Leu Ile Gly Gln Met Arg Asp Val Ile Gly Ala Ala 435 440 445			
Thr Ala Asn Gln Asn Tyr Phe Arg Ala Cys Met Asp Asp Thr Ile Ala 450 455 460			
Tyr Met Asn Asn Tyr Ser Ile Pro Lys Leu Val Gln Lys Arg Val Arg 465 470 475 480			
Thr Trp Tyr Glu Tyr Thr Trp Asp Ser Gln Arg Met Leu Asp Glu Ser 485 490 495			
Asp Leu Leu Lys Thr Leu Pro Thr Thr Val Gln Leu Ala Leu Ala Ile 500 505 510			
Asp Val Asn Phe Ser Ile Ile Ser Lys Val Asp Leu Phe Lys Gly Cys 515 520 525			
Asp Thr Gln Met Ile Tyr Asp Met Leu Leu Arg Leu Lys Ser Val Leu 530 535 540			
Tyr Leu Pro Gly Asp Phe Val Cys Lys Lys Gly Glu Ile Gly Lys Glu 545 550 555 560			
Met Tyr Ile Ile Lys His Gly Glu Val Gln Val Leu Gly Gly Pro Asp 565 570 575			
Gly Thr Lys Val Leu Val Thr Leu Lys Ala Gly Ser Val Phe Gly Glu 580 585 590			
Ile Ser Leu Leu Ala Ala Gly Gly Gly Asn Arg Arg Thr Ala Asn Val 595 600 605			
Val Ala His Gly Phe Ala Asn Leu Leu Thr Leu Asp Lys Lys Thr Leu 610 615 620			
Gln Glu Ile Leu Val His Tyr Pro Asp Ser Glu Arg Ile Leu Met Lys 625 630 635 640			
Lys Ala Arg Val Leu Leu Lys Gln Lys Ala Lys Thr Ala Glu Ala Thr 645 650 655			
Pro Pro Arg Lys Asp Leu Ala Leu Leu Phe Pro Pro Lys Glu Glu Thr 660 665 670			
Pro Lys Leu Phe Lys Thr Leu Leu Gly Gly Thr Gly Lys Ala Ser Leu 675 680 685			
Ala Arg Leu Leu Lys Leu Lys Arg Glu Gln Ala Ala Gln Lys Lys Glu 690 695 700			
Asn Ser Glu Gly Gly Glu Glu Glu Gly Lys Glu Asn Glu Asp Lys Gln 705 710 715 720			
Lys Glu Asn Glu Asp Lys Gln Lys Glu Asn Glu Asp Lys Gly Lys Glu 725 730 735			

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Asn Glu Asp Lys Asp Lys Gly Arg Glu Pro Glu Glu Lys Pro Leu Asp  
 740 745 750

Arg Pro Glu Cys Thr Ala Ser Pro Ile Ala Val Glu Glu Glu Pro His  
 755 760 765

Ser Val Arg Arg Thr Val Leu Pro Arg Gly Thr Ser Arg Gln Ser Leu  
 770 775 780

Ile Ile Ser Met Ala Pro Ser Ala Glu Gly Gly Glu Glu Val Leu Thr  
 785 790 795 800

Ile Glu Val Lys Glu Lys Ala Lys Gln  
 805

&lt;210&gt; SEQ ID NO 27

&lt;211&gt; LENGTH: 354

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 27

Met Gly Ser Gly Ala Ser Ala Glu Asp Lys Glu Leu Ala Lys Arg Ser  
 1 5 10 15

Lys Glu Leu Glu Lys Lys Leu Gln Glu Asp Ala Asp Lys Glu Ala Lys  
 20 25 30

Thr Val Lys Leu Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr  
 35 40 45

Ile Val Lys Gln Met Lys Ile Ile His Gln Asp Gly Tyr Ser Pro Glu  
 50 55 60

Glu Cys Leu Glu Phe Lys Ala Ile Ile Tyr Gly Asn Val Leu Gln Ser  
 65 70 75 80

Ile Leu Ala Ile Ile Arg Ala Met Thr Thr Leu Gly Ile Asp Tyr Ala  
 85 90 95

Glu Pro Ser Cys Ala Asp Asp Gly Arg Gln Leu Asn Asn Leu Ala Asp  
 100 105 110

Ser Ile Glu Glu Gly Thr Met Pro Pro Glu Leu Val Glu Val Ile Arg  
 115 120 125

Arg Leu Trp Lys Asp Gly Gly Val Gln Ala Cys Phe Glu Arg Ala Ala  
 130 135 140

Glu Tyr Gln Leu Asn Asp Ser Ala Ser Tyr Tyr Leu Asn Gln Leu Glu  
 145 150 155 160

Arg Ile Thr Asp Pro Glu Tyr Leu Pro Ser Glu Gln Asp Val Leu Arg  
 165 170 175

Ser Arg Val Lys Thr Thr Gly Ile Ile Glu Thr Lys Phe Ser Val Lys  
 180 185 190

Asp Leu Asn Phe Arg Met Phe Asp Val Gly Gly Gln Arg Ser Glu Arg  
 195 200 205

Lys Lys Trp Ile His Cys Phe Glu Gly Val Thr Cys Ile Ile Phe Cys  
 210 215 220

Ala Ala Leu Ser Ala Tyr Asp Met Val Leu Val Glu Asp Asp Glu Val  
 225 230 235 240

Asn Arg Met His Glu Ser Leu His Leu Phe Asn Ser Ile Cys Asn His  
 245 250 255

Lys Phe Phe Ala Ala Thr Ser Ile Val Leu Phe Leu Asn Lys Lys Asp  
 260 265 270

Leu Phe Glu Glu Lys Ile Lys Lys Val His Leu Ser Ile Cys Phe Pro  
 275 280 285

Glu Tyr Asp Gly Asn Asn Ser Tyr Asp Asp Ala Gly Asn Tyr Ile Lys

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290                      295                      300

Ser Gln Phe Leu Asp Leu Asn Met Arg Lys Asp Val Lys Glu Ile Tyr  
305                      310                      315                      320

Ser His Met Thr Cys Ala Thr Asp Thr Gln Asn Val Lys Phe Val Phe  
                            325                      330                      335

Asp Ala Val Thr Asp Ile Ile Ile Lys Glu Asn Leu Lys Asp Cys Gly  
                            340                      345                      350

Leu Phe

<210> SEQ ID NO 28  
<211> LENGTH: 815  
<212> TYPE: PRT  
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 28

Met Arg Glu Pro Glu Glu Leu Met Pro Asp Ser Gly Ala Val Phe Thr  
1                      5                      10                      15

Phe Gly Lys Ser Lys Phe Ala Glu Asn Asn Pro Gly Lys Phe Trp Phe  
                            20                      25                      30

Lys Asn Asp Val Pro Val His Leu Ser Cys Gly Asp Glu His Ser Ala  
                            35                      40                      45

Val Val Thr Gly Asn Asn Lys Leu Tyr Met Phe Gly Ser Asn Asn Trp  
                            50                      55                      60

Gly Gln Leu Gly Leu Gly Ser Lys Ser Ala Ile Ser Lys Pro Thr Cys  
65                      70                      75                      80

Val Lys Ala Leu Lys Pro Glu Lys Val Lys Leu Ala Ala Cys Gly Arg  
                            85                      90                      95

Asn His Thr Leu Val Ser Thr Glu Gly Gly Asn Val Tyr Ala Thr Gly  
                            100                      105                      110

Gly Asn Asn Glu Gly Gln Leu Gly Leu Gly Asp Thr Glu Glu Arg Asn  
                            115                      120                      125

Thr Phe His Val Ile Ser Phe Phe Thr Ser Glu His Lys Ile Lys Gln  
130                      135                      140

Leu Ser Ala Gly Ser Asn Thr Ser Ala Ala Leu Thr Glu Asp Gly Arg  
145                      150                      155                      160

Leu Phe Met Trp Gly Asp Asn Ser Glu Gly Gln Ile Gly Leu Lys Asn  
                            165                      170                      175

Val Ser Asn Val Cys Val Pro Gln Gln Val Thr Ile Gly Lys Pro Val  
                            180                      185                      190

Ser Trp Ile Ser Cys Gly Tyr Tyr His Ser Ala Phe Val Thr Thr Asp  
                            195                      200                      205

Gly Glu Leu Tyr Val Phe Gly Glu Pro Glu Asn Gly Lys Leu Gly Leu  
210                      215                      220

Pro Asn Gln Leu Leu Gly Asn His Arg Thr Pro Gln Leu Val Ser Glu  
225                      230                      235                      240

Ile Pro Glu Lys Val Ile Gln Val Ala Cys Gly Gly Glu His Thr Val  
                            245                      250                      255

Val Leu Thr Glu Asn Ala Val Tyr Thr Phe Gly Leu Gly Gln Phe Gly  
                            260                      265                      270

Gln Leu Gly Leu Gly Thr Phe Leu Phe Glu Thr Ser Glu Pro Lys Val  
                            275                      280                      285

Ile Glu Asn Ile Arg Asp Gln Thr Ile Ser Tyr Ile Ser Cys Gly Glu  
290                      295                      300

Asn His Thr Ala Leu Ile Thr Asp Ile Gly Leu Met Tyr Thr Phe Gly

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305	310	315	320
Asp Gly Arg His Gly Lys Leu Gly Leu Gly Leu Glu Asn Phe Thr Asn 325 330 335			
His Phe Ile Pro Thr Leu Cys Ser Asn Phe Leu Arg Phe Ile Val Lys 340 345 350			
Leu Val Ala Cys Gly Gly Cys His Met Val Val Phe Ala Ala Pro His 355 360 365			
Arg Gly Val Ala Lys Glu Ile Glu Phe Asp Glu Ile Asn Asp Thr Cys 370 375 380			
Leu Ser Val Ala Thr Phe Leu Pro Tyr Ser Ser Leu Thr Ser Gly Asn 385 390 395 400			
Val Leu Gln Arg Thr Leu Ser Ala Arg Met Arg Arg Arg Glu Arg Glu 405 410 415			
Arg Ser Pro Asp Ser Phe Ser Met Arg Arg Thr Leu Pro Pro Ile Glu 420 425 430			
Gly Thr Leu Gly Leu Ser Ala Cys Phe Leu Pro Asn Ser Val Phe Pro 435 440 445			
Arg Cys Ser Glu Arg Asn Leu Gln Glu Ser Val Leu Ser Glu Gln Asp 450 455 460			
Leu Met Gln Pro Glu Glu Pro Asp Tyr Leu Leu Asp Glu Met Thr Lys 465 470 475 480			
Glu Ala Glu Ile Asp Asn Ser Ser Thr Val Glu Ser Leu Gly Glu Thr 485 490 495			
Thr Asp Ile Leu Asn Met Thr His Ile Met Ser Leu Asn Ser Asn Glu 500 505 510			
Lys Ser Leu Lys Leu Ser Pro Val Gln Lys Gln Lys Lys Gln Gln Thr 515 520 525			
Ile Gly Glu Leu Thr Gln Asp Thr Ala Leu Thr Glu Asn Asp Asp Ser 530 535 540			
Asp Glu Tyr Glu Glu Met Ser Glu Met Lys Glu Gly Lys Ala Cys Lys 545 550 555 560			
Gln His Val Ser Gln Gly Ile Phe Met Thr Gln Pro Ala Thr Thr Ile 565 570 575			
Glu Ala Phe Ser Asp Glu Glu Val Glu Ile Pro Glu Glu Lys Glu Gly 580 585 590			
Ala Glu Asp Ser Lys Gly Asn Gly Ile Glu Glu Gln Glu Val Glu Ala 595 600 605			
Asn Glu Glu Asn Val Lys Val His Gly Gly Arg Lys Glu Lys Thr Glu 610 615 620			
Ile Leu Ser Asp Asp Leu Thr Asp Lys Ala Glu Asp His Glu Phe Ser 625 630 635 640			
Lys Thr Glu Glu Leu Lys Leu Glu Asp Val Asp Glu Glu Ile Asn Ala 645 650 655			
Glu Asn Val Glu Ser Lys Lys Lys Thr Val Gly Asp Asp Glu Ser Val 660 665 670			
Pro Thr Gly Tyr His Ser Lys Thr Glu Gly Ala Glu Arg Thr Asn Asp 675 680 685			
Asp Ser Ser Ala Glu Thr Ile Glu Lys Lys Glu Lys Ala Asn Leu Glu 690 695 700			
Glu Arg Ala Ile Cys Glu Tyr Asn Glu Asn Pro Lys Gly Tyr Met Leu 705 710 715 720			
Asp Asp Ala Asp Ser Ser Ser Leu Glu Ile Leu Glu Asn Ser Glu Thr 725 730 735			

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Thr Pro Ser Lys Asp Met Lys Lys Thr Lys Lys Ile Phe Leu Phe Lys  
 740 745 750  
 Arg Val Pro Ser Ile Asn Gln Lys Ile Val Lys Asn Asn Asn Glu Pro  
 755 760 765  
 Leu Pro Glu Ile Lys Ser Ile Gly Asp Gln Ile Ile Leu Lys Ser Asp  
 770 775 780  
 Asn Lys Asp Ala Asp Gln Asn His Met Ser Gln Asn His Gln Asn Ile  
 785 790 795 800  
 Pro Pro Thr Asn Thr Glu Arg Arg Ser Lys Ser Cys Thr Ile Leu  
 805 810 815

<210> SEQ ID NO 29  
 <211> LENGTH: 646  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 29

Met Arg Glu Pro Glu Glu Leu Met Pro Asp Ser Gly Ala Val Phe Thr  
 1 5 10 15  
 Phe Gly Lys Ser Lys Phe Ala Glu Asn Asn Pro Gly Lys Phe Trp Phe  
 20 25 30  
 Lys Asn Asp Val Pro Val His Leu Ser Cys Gly Asp Glu His Ser Ala  
 35 40 45  
 Val Val Thr Gly Asn Asn Lys Leu Tyr Met Phe Gly Ser Asn Asn Trp  
 50 55 60  
 Gly Gln Leu Gly Leu Gly Ser Lys Ser Ala Ile Ser Lys Pro Thr Cys  
 65 70 75 80  
 Val Lys Ala Leu Lys Pro Glu Lys Val Lys Leu Ala Ala Cys Gly Arg  
 85 90 95  
 Asn His Thr Leu Val Ser Thr Glu Gly Gly Asn Val Tyr Ala Thr Gly  
 100 105 110  
 Gly Asn Asn Glu Gly Gln Leu Gly Leu Gly Asp Thr Glu Glu Arg Asn  
 115 120 125  
 Thr Phe His Val Ile Ser Phe Phe Thr Ser Glu His Lys Ile Lys Gln  
 130 135 140  
 Leu Ser Ala Gly Ser Asn Thr Ser Ala Ala Leu Thr Glu Asp Gly Arg  
 145 150 155 160  
 Leu Phe Met Trp Gly Asp Asn Ser Glu Gly Gln Ile Gly Leu Lys Asn  
 165 170 175  
 Val Ser Asn Val Cys Val Pro Gln Gln Val Thr Ile Gly Lys Pro Val  
 180 185 190  
 Ser Trp Ile Ser Cys Gly Tyr Tyr His Ser Ala Phe Val Thr Thr Asp  
 195 200 205  
 Gly Glu Leu Tyr Val Phe Gly Glu Pro Glu Asn Gly Lys Leu Gly Leu  
 210 215 220  
 Pro Asn Gln Leu Leu Gly Asn His Arg Thr Pro Gln Leu Val Ser Glu  
 225 230 235 240  
 Ile Pro Glu Lys Val Ile Gln Val Ala Cys Gly Gly Glu His Thr Val  
 245 250 255  
 Val Leu Thr Glu Asn Ala Val Tyr Thr Phe Gly Leu Gly Gln Phe Gly  
 260 265 270  
 Gln Leu Gly Leu Gly Thr Phe Leu Phe Glu Thr Ser Glu Pro Lys Val  
 275 280 285  
 Ile Glu Asn Ile Arg Asp Gln Thr Ile Ser Tyr Ile Ser Cys Gly Glu

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290	295	300
Asn His Thr Ala Leu Ile Thr Asp Ile Gly Leu Met Tyr Thr Phe Gly 305	310	315
Asp Gly Arg His Gly Lys Leu Gly Leu Gly Leu Glu Asn Phe Thr Asn 325	330	335
His Phe Ile Pro Thr Leu Cys Ser Asn Phe Leu Arg Phe Ile Val Lys 340	345	350
Leu Val Ala Cys Gly Gly Cys His Met Val Val Phe Ala Ala Pro His 355	360	365
Arg Gly Val Ala Lys Glu Ile Glu Phe Asp Glu Ile Asn Asp Thr Cys 370	375	380
Leu Ser Val Ala Thr Phe Leu Pro Tyr Ser Ser Leu Thr Ser Gly Asn 385	390	395
Val Leu Gln Arg Thr Leu Ser Ala Arg Met Arg Arg Arg Glu Arg Glu 405	410	415
Arg Ser Pro Asp Ser Phe Ser Met Arg Arg Thr Leu Pro Pro Ile Glu 420	425	430
Gly Thr Leu Gly Leu Ser Ala Cys Phe Leu Pro Asn Ser Val Phe Pro 435	440	445
Arg Cys Ser Glu Arg Asn Leu Gln Glu Ser Val Leu Ser Glu Gln Asp 450	455	460
Leu Met Gln Pro Glu Glu Pro Asp Tyr Leu Leu Asp Glu Met Thr Lys 465	470	475
Glu Ala Glu Ile Asp Asn Ser Ser Thr Val Glu Ser Leu Gly Glu Thr 485	490	495
Thr Asp Ile Leu Asn Met Thr His Ile Met Ser Leu Asn Ser Asn Glu 500	505	510
Lys Ser Leu Lys Leu Ser Pro Val Gln Lys Gln Lys Lys Gln Gln Thr 515	520	525
Ile Gly Glu Leu Thr Gln Asp Thr Ala Leu Thr Glu Asn Asp Asp Ser 530	535	540
Asp Glu Tyr Glu Glu Met Ser Glu Met Lys Glu Gly Lys Ala Cys Lys 545	550	555
Gln His Val Ser Gln Gly Ile Phe Met Thr Gln Pro Ala Thr Thr Ile 565	570	575
Glu Ala Phe Ser Asp Glu Glu Val Glu Ile Pro Glu Glu Lys Glu Gly 580	585	590
Ala Glu Asp Ser Lys Gly Asn Gly Ile Glu Glu Gln Glu Val Glu Ala 595	600	605
Asn Glu Glu Asn Val Lys Val His Gly Gly Arg Lys Glu Lys Thr Glu 610	615	620
Ile Leu Ser Asp Asp Leu Thr Asp Lys Ala Glu Tyr Ser Ala Ser His 625	630	635
Ser Gln Ile Val Ser Val 645		

&lt;210&gt; SEQ ID NO 30

&lt;211&gt; LENGTH: 1152

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Homo sapiens

&lt;400&gt; SEQUENCE: 30

Met Arg Glu Pro Glu Glu Leu Met Pro Asp Ser Gly Ala Val Phe Thr 1	5	10	15
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Phe	Gly	Lys	Ser	Lys	Phe	Ala	Glu	Asn	Asn	Pro	Gly	Lys	Phe	Trp	Phe
			20					25					30		
Lys	Asn	Asp	Val	Pro	Val	His	Leu	Ser	Cys	Gly	Asp	Glu	His	Ser	Ala
		35					40					45			
Val	Val	Thr	Gly	Asn	Asn	Lys	Leu	Tyr	Met	Phe	Gly	Ser	Asn	Asn	Trp
	50					55					60				
Gly	Gln	Leu	Gly	Leu	Gly	Ser	Lys	Ser	Ala	Ile	Ser	Lys	Pro	Thr	Cys
65					70					75					80
Val	Lys	Ala	Leu	Lys	Pro	Glu	Lys	Val	Lys	Leu	Ala	Ala	Cys	Gly	Arg
				85					90					95	
Asn	His	Thr	Leu	Val	Ser	Thr	Glu	Gly	Gly	Asn	Val	Tyr	Ala	Thr	Gly
			100					105					110		
Gly	Asn	Asn	Glu	Gly	Gln	Leu	Gly	Leu	Gly	Asp	Thr	Glu	Glu	Arg	Asn
		115					120					125			
Thr	Phe	His	Val	Ile	Ser	Phe	Phe	Thr	Ser	Glu	His	Lys	Ile	Lys	Gln
	130					135					140				
Leu	Ser	Ala	Gly	Ser	Asn	Thr	Ser	Ala	Ala	Leu	Thr	Glu	Asp	Gly	Arg
145					150					155					160
Leu	Phe	Met	Trp	Gly	Asp	Asn	Ser	Glu	Gly	Gln	Ile	Gly	Leu	Lys	Asn
				165					170					175	
Val	Ser	Asn	Val	Cys	Val	Pro	Gln	Gln	Val	Thr	Ile	Gly	Lys	Pro	Val
			180					185					190		
Ser	Trp	Ile	Ser	Cys	Gly	Tyr	Tyr	His	Ser	Ala	Phe	Val	Thr	Thr	Asp
		195					200					205			
Gly	Glu	Leu	Tyr	Val	Phe	Gly	Glu	Pro	Glu	Asn	Gly	Lys	Leu	Gly	Leu
	210					215					220				
Pro	Asn	Gln	Leu	Leu	Gly	Asn	His	Arg	Thr	Pro	Gln	Leu	Val	Ser	Glu
225					230					235					240
Ile	Pro	Glu	Lys	Val	Ile	Gln	Val	Ala	Cys	Gly	Gly	Glu	His	Thr	Val
				245					250					255	
Val	Leu	Thr	Glu	Asn	Ala	Val	Tyr	Thr	Phe	Gly	Leu	Gly	Gln	Phe	Gly
			260					265					270		
Gln	Leu	Gly	Leu	Gly	Thr	Phe	Leu	Phe	Glu	Thr	Ser	Glu	Pro	Lys	Val
		275					280					285			
Ile	Glu	Asn	Ile	Arg	Asp	Gln	Thr	Ile	Ser	Tyr	Ile	Ser	Cys	Gly	Glu
	290					295					300				
Asn	His	Thr	Ala	Leu	Ile	Thr	Asp	Ile	Gly	Leu	Met	Tyr	Thr	Phe	Gly
305					310					315					320
Asp	Gly	Arg	His	Gly	Lys	Leu	Gly	Leu	Gly	Leu	Glu	Asn	Phe	Thr	Asn
				325					330					335	
His	Phe	Ile	Pro	Thr	Leu	Cys	Ser	Asn	Phe	Leu	Arg	Phe	Ile	Val	Lys
			340					345					350		
Leu	Val	Ala	Cys	Gly	Gly	Cys	His	Met	Val	Val	Phe	Ala	Ala	Pro	His
		355					360					365			
Arg	Gly	Val	Ala	Lys	Glu	Ile	Glu	Phe	Asp	Glu	Ile	Asn	Asp	Thr	Cys
	370					375					380				
Leu	Ser	Val	Ala	Thr	Phe	Leu	Pro	Tyr	Ser	Ser	Leu	Thr	Ser	Gly	Asn
385					390					395					400
Val	Leu	Gln	Arg	Thr	Leu	Ser	Ala	Arg	Met	Arg	Arg	Arg	Glu	Arg	Glu
				405					410					415	
Arg	Ser	Pro	Asp	Ser	Phe	Ser	Met	Arg	Arg	Thr	Leu	Pro	Pro	Ile	Glu
			420					425					430		
Gly	Thr	Leu	Gly	Leu	Ser	Ala	Cys	Phe	Leu	Pro	Asn	Ser	Val	Phe	Pro



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435				440				445							
Arg	Cys	Ser	Glu	Arg	Asn	Leu	Gln	Glu	Ser	Val	Leu	Ser	Glu	Gln	Asp
	450					455					460				
Leu	Met	Gln	Pro	Glu	Glu	Pro	Asp	Tyr	Leu	Leu	Asp	Glu	Met	Thr	Lys
465					470					475					480
Glu	Ala	Glu	Ile	Asp	Asn	Ser	Ser	Thr	Val	Glu	Ser	Leu	Gly	Glu	Thr
				485					490					495	
Thr	Asp	Ile	Leu	Asn	Met	Thr	His	Ile	Met	Ser	Leu	Asn	Ser	Asn	Glu
			500					505						510	
Lys	Ser	Leu	Lys	Leu	Ser	Pro	Val	Gln	Lys	Gln	Lys	Lys	Gln	Gln	Thr
		515					520							525	
Ile	Gly	Glu	Leu	Thr	Gln	Asp	Thr	Ala	Leu	Thr	Glu	Asn	Asp	Asp	Ser
	530					535					540				
Asp	Glu	Tyr	Glu	Glu	Met	Ser	Glu	Met	Lys	Glu	Gly	Lys	Ala	Cys	Lys
545					550					555					560
Gln	His	Val	Ser	Gln	Gly	Ile	Phe	Met	Thr	Gln	Pro	Ala	Thr	Thr	Ile
				565					570						575
Glu	Ala	Phe	Ser	Asp	Glu	Glu	Val	Glu	Ile	Pro	Glu	Glu	Lys	Glu	Gly
			580					585					590		
Ala	Glu	Asp	Ser	Lys	Gly	Asn	Gly	Ile	Glu	Glu	Gln	Glu	Val	Glu	Ala
		595					600						605		
Asn	Glu	Glu	Asn	Val	Lys	Val	His	Gly	Gly	Arg	Lys	Glu	Lys	Thr	Glu
	610					615					620				
Ile	Leu	Ser	Asp	Asp	Leu	Thr	Asp	Lys	Ala	Glu	Val	Ser	Glu	Gly	Lys
625					630					635					640
Ala	Lys	Ser	Val	Gly	Glu	Ala	Glu	Asp	Gly	Pro	Glu	Gly	Arg	Gly	Asp
				645					650					655	
Gly	Thr	Cys	Glu	Glu	Gly	Ser	Ser	Gly	Ala	Glu	His	Trp	Gln	Asp	Glu
			660					665					670		
Glu	Arg	Glu	Lys	Gly	Glu	Lys	Asp	Lys	Gly	Arg	Gly	Glu	Met	Glu	Arg
		675					680						685		
Pro	Gly	Glu	Gly	Glu	Lys	Glu	Leu	Ala	Glu	Lys	Glu	Glu	Trp	Lys	Lys
	690					695					700				
Arg	Asp	Gly	Glu	Glu	Gln	Glu	Gln	Lys	Glu	Arg	Glu	Gln	Gly	His	Gln
705					710					715					720
Lys	Glu	Arg	Asn	Gln	Glu	Met	Glu	Glu	Gly	Gly	Glu	Glu	Glu	His	Gly
				725					730					735	
Glu	Gly	Glu	Glu	Glu	Glu	Gly	Asp	Arg	Glu	Glu	Glu	Glu	Glu	Lys	Glu
			740					745					750		
Gly	Glu	Gly	Lys	Glu	Glu	Gly	Glu	Gly	Glu	Glu	Val	Glu	Gly	Glu	Arg
		755					760						765		
Glu	Lys	Glu	Glu	Gly	Glu	Arg	Lys	Lys	Glu	Glu	Arg	Ala	Gly	Lys	Glu
		770				775					780				
Glu	Lys	Gly	Glu	Glu	Glu	Gly	Asp	Gln	Gly	Glu	Gly	Glu	Glu	Glu	Glu
785					790					795					800
Thr	Glu	Gly	Arg	Gly	Glu	Glu	Lys	Glu	Glu	Gly	Gly	Glu	Val	Glu	Gly
				805					810					815	
Gly	Glu	Val	Glu	Glu	Gly	Lys	Gly	Glu	Arg	Glu	Glu	Glu	Glu	Glu	Glu
			820					825					830		
Gly	Glu	Gly	Glu	Glu	Glu	Glu	Gly	Glu	Gly	Glu	Glu	Glu	Glu	Gly	Glu
		835					840						845		
Gly	Glu	Glu	Glu	Glu	Gly	Glu	Gly	Lys	Gly	Glu	Glu	Glu	Gly	Glu	Glu
		850				855					860				

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Gly Glu Gly Glu Glu Glu Gly Glu Glu Gly Glu Gly Glu Gly Glu Glu  
 865 870 875 880  
 Glu Glu Gly Glu Gly Glu Gly Glu Glu Glu Gly Glu Gly Glu Gly Glu  
 885 890 895  
 Glu Glu Glu Gly Glu Gly Glu Gly Glu Glu Gly Glu Gly Glu Gly  
 900 905 910  
 Glu Glu Glu Glu Gly Glu Gly Lys Gly Glu Glu Glu Gly Glu Glu Gly  
 915 920 925  
 Glu Gly Glu Gly Glu Glu Glu Glu Gly Glu Gly Glu Gly Glu Asp Gly  
 930 935 940  
 Glu Gly Glu Gly Glu Glu Glu Glu Gly Glu Trp Glu Gly Glu Glu Glu  
 945 950 955 960  
 Glu Gly Glu Gly Glu Gly Glu Glu Glu Gly Glu Gly Glu Gly Glu Glu  
 965 970 975  
 Gly Glu Gly Glu Gly Glu Glu Glu Glu Gly Glu Gly Glu Gly Glu Glu  
 980 985 990  
 Glu Glu Gly Glu Glu Glu Gly Glu Glu Glu Gly Glu Gly Glu Glu Glu  
 995 1000 1005  
 Gly Glu Gly Glu Gly Glu Glu Glu Glu Glu Gly Glu Val Glu Gly  
 1010 1015 1020  
 Glu Val Glu Gly Glu Glu Gly Glu Gly Glu Gly Glu Glu Glu Glu  
 1025 1030 1035  
 Gly Glu Glu Glu Gly Glu Glu Arg Glu Lys Glu Gly Glu Gly Glu  
 1040 1045 1050  
 Glu Asn Arg Arg Asn Arg Glu Glu Glu Glu Glu Glu Glu Gly Lys  
 1055 1060 1065  
 Tyr Gln Glu Thr Gly Glu Glu Glu Asn Glu Arg Gln Asp Gly Glu  
 1070 1075 1080  
 Glu Tyr Lys Lys Val Ser Lys Ile Lys Gly Ser Val Lys Tyr Gly  
 1085 1090 1095  
 Lys His Lys Thr Tyr Gln Lys Lys Ser Val Thr Asn Thr Gln Gly  
 1100 1105 1110  
 Asn Gly Lys Glu Gln Arg Ser Lys Met Pro Val Gln Ser Lys Arg  
 1115 1120 1125  
 Leu Leu Lys Asn Gly Pro Ser Gly Ser Lys Lys Phe Trp Asn Asn  
 1130 1135 1140  
 Val Leu Pro His Tyr Leu Glu Leu Lys  
 1145 1150

<210> SEQ ID NO 31  
 <211> LENGTH: 1020  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 31

Met Arg Glu Pro Glu Glu Leu Met Pro Asp Ser Gly Ala Val Phe Thr  
 1 5 10 15  
 Phe Gly Lys Ser Lys Phe Ala Glu Asn Asn Pro Gly Lys Phe Trp Phe  
 20 25 30  
 Lys Asn Asp Val Pro Val His Leu Ser Cys Gly Asp Glu His Ser Ala  
 35 40 45  
 Val Val Thr Gly Asn Asn Lys Leu Tyr Met Phe Gly Ser Asn Asn Trp  
 50 55 60  
 Gly Gln Leu Gly Leu Gly Ser Lys Ser Ala Ile Ser Lys Pro Thr Cys

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65	70	75	80
Val Lys Ala Leu Lys Pro Glu Lys Val Lys Leu Ala Ala Cys Gly Arg 85 90 95			
Asn His Thr Leu Val Ser Thr Glu Gly Gly Asn Val Tyr Ala Thr Gly 100 105 110			
Gly Asn Asn Glu Gly Gln Leu Gly Leu Gly Asp Thr Glu Glu Arg Asn 115 120 125			
Thr Phe His Val Ile Ser Phe Phe Thr Ser Glu His Lys Ile Lys Gln 130 135 140			
Leu Ser Ala Gly Ser Asn Thr Ser Ala Ala Leu Thr Glu Asp Gly Arg 145 150 155 160			
Leu Phe Met Trp Gly Asp Asn Ser Glu Gly Gln Ile Gly Leu Lys Asn 165 170 175			
Val Ser Asn Val Cys Val Pro Gln Gln Val Thr Ile Gly Lys Pro Val 180 185 190			
Ser Trp Ile Ser Cys Gly Tyr Tyr His Ser Ala Phe Val Thr Thr Asp 195 200 205			
Gly Glu Leu Tyr Val Phe Gly Glu Pro Glu Asn Gly Lys Leu Gly Leu 210 215 220			
Pro Asn Gln Leu Leu Gly Asn His Arg Thr Pro Gln Leu Val Ser Glu 225 230 235 240			
Ile Pro Glu Lys Val Ile Gln Val Ala Cys Gly Gly Glu His Thr Val 245 250 255			
Val Leu Thr Glu Asn Ala Val Tyr Thr Phe Gly Leu Gly Gln Phe Gly 260 265 270			
Gln Leu Gly Leu Gly Thr Phe Leu Phe Glu Thr Ser Glu Pro Lys Val 275 280 285			
Ile Glu Asn Ile Arg Asp Gln Thr Ile Ser Tyr Ile Ser Cys Gly Glu 290 295 300			
Asn His Thr Ala Leu Ile Thr Asp Ile Gly Leu Met Tyr Thr Phe Gly 305 310 315 320			
Asp Gly Arg His Gly Lys Leu Gly Leu Gly Leu Glu Asn Phe Thr Asn 325 330 335			
His Phe Ile Pro Thr Leu Cys Ser Asn Phe Leu Arg Phe Ile Val Lys 340 345 350			
Leu Val Ala Cys Gly Gly Cys His Met Val Val Phe Ala Ala Pro His 355 360 365			
Arg Gly Val Ala Lys Glu Ile Glu Phe Asp Glu Ile Asn Asp Thr Cys 370 375 380			
Leu Ser Val Ala Thr Phe Leu Pro Tyr Ser Ser Leu Thr Ser Gly Asn 385 390 395 400			
Val Leu Gln Arg Thr Leu Ser Ala Arg Met Arg Arg Arg Glu Arg Glu 405 410 415			
Arg Ser Pro Asp Ser Phe Ser Met Arg Arg Thr Leu Pro Pro Ile Glu 420 425 430			
Gly Thr Leu Gly Leu Ser Ala Cys Phe Leu Pro Asn Ser Val Phe Pro 435 440 445			
Arg Cys Ser Glu Arg Asn Leu Gln Glu Ser Val Leu Ser Glu Gln Asp 450 455 460			
Leu Met Gln Pro Glu Glu Pro Asp Tyr Leu Leu Asp Glu Met Thr Lys 465 470 475 480			
Glu Ala Glu Ile Asp Asn Ser Ser Thr Val Glu Ser Leu Gly Glu Thr 485 490 495			

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Thr Asp Ile Leu Asn Met Thr His Ile Met Ser Leu Asn Ser Asn Glu  
 500 505 510

Lys Ser Leu Lys Leu Ser Pro Val Gln Lys Gln Lys Lys Gln Gln Thr  
 515 520 525

Ile Gly Glu Leu Thr Gln Asp Thr Ala Leu Thr Glu Asn Asp Asp Ser  
 530 535 540

Asp Glu Tyr Glu Glu Met Ser Glu Met Lys Glu Gly Lys Ala Cys Lys  
 545 550 555 560

Gln His Val Ser Gln Gly Ile Phe Met Thr Gln Pro Ala Thr Thr Ile  
 565 570 575

Glu Ala Phe Ser Asp Glu Glu Val Gly Asn Asp Thr Gly Gln Val Gly  
 580 585 590

Pro Gln Ala Asp Thr Asp Gly Glu Gly Leu Gln Lys Glu Val Tyr Arg  
 595 600 605

His Glu Asn Asn Asn Gly Val Asp Gln Leu Asp Ala Lys Glu Ile Glu  
 610 615 620

Lys Glu Ser Asp Gly Gly His Ser Gln Lys Glu Ser Glu Ala Glu Glu  
 625 630 635 640

Ile Asp Ser Glu Lys Glu Thr Lys Leu Ala Glu Ile Ala Gly Met Lys  
 645 650 655

Asp Leu Arg Glu Arg Glu Lys Ser Thr Lys Lys Met Ser Pro Phe Phe  
 660 665 670

Gly Asn Leu Pro Asp Arg Gly Met Asn Thr Glu Ser Glu Glu Asn Lys  
 675 680 685

Asp Phe Val Lys Lys Arg Glu Ser Cys Lys Gln Asp Val Ile Phe Asp  
 690 695 700

Ser Glu Arg Glu Ser Val Glu Lys Pro Asp Ser Tyr Met Glu Gly Ala  
 705 710 715 720

Ser Glu Ser Gln Gln Gly Ile Ala Asp Gly Phe Gln Gln Pro Glu Ala  
 725 730 735

Ile Glu Phe Ser Ser Gly Glu Lys Glu Asp Asp Glu Val Glu Thr Asp  
 740 745 750

Gln Asn Ile Arg Tyr Gly Arg Lys Leu Ile Glu Gln Gly Asn Glu Lys  
 755 760 765

Glu Thr Lys Pro Ile Ile Ser Lys Ser Met Ala Lys Tyr Asp Phe Lys  
 770 775 780

Cys Asp Arg Leu Ser Glu Ile Pro Glu Glu Lys Glu Gly Ala Glu Asp  
 785 790 795 800

Ser Lys Gly Asn Gly Ile Glu Glu Gln Glu Val Glu Ala Asn Glu Glu  
 805 810 815

Asn Val Lys Val His Gly Gly Arg Lys Glu Lys Thr Glu Ile Leu Ser  
 820 825 830

Asp Asp Leu Thr Asp Lys Ala Glu Asp His Glu Phe Ser Lys Thr Glu  
 835 840 845

Glu Leu Lys Leu Glu Asp Val Asp Glu Glu Ile Asn Ala Glu Asn Val  
 850 855 860

Glu Ser Lys Lys Lys Thr Val Gly Asp Asp Glu Ser Val Pro Thr Gly  
 865 870 875 880

Tyr His Ser Lys Thr Glu Gly Ala Glu Arg Thr Asn Asp Asp Ser Ser  
 885 890 895

Ala Glu Thr Ile Glu Lys Lys Glu Lys Ala Asn Leu Glu Glu Arg Ala  
 900 905 910

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Ile Cys Glu Tyr Asn Glu Asn Pro Lys Gly Tyr Met Leu Asp Asp Ala
    915                                920                                925

Asp Ser Ser Ser Leu Glu Ile Leu Glu Asn Ser Glu Thr Thr Pro Ser
    930                                935                                940

Lys Asp Met Lys Lys Thr Lys Lys Ile Phe Leu Phe Lys Arg Val Pro
    945                                950                                955                                960

Ser Ile Asn Gln Lys Ile Val Lys Asn Asn Asn Glu Pro Leu Pro Glu
    965                                970                                975

Ile Lys Ser Ile Gly Asp Gln Ile Ile Leu Lys Ser Asp Asn Lys Asp
    980                                985                                990

Ala Asp Gln Asn His Met Ser Gln Asn His Gln Asn Ile Pro Pro Thr
    995                                1000                                1005

Asn Thr Glu Arg Arg Ser Lys Ser Cys Thr Ile Leu
    1010                                1015                                1020

<210> SEQ ID NO 32
<211> LENGTH: 1368
<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 32

Met Asp Lys Lys Tyr Ser Ile Gly Leu Asp Ile Gly Thr Asn Ser Val
 1      5      10      15

Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
 20     25     30

Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
 35     40     45

Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
 50     55     60

Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
 65     70     75     80

Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
 85     90     95

Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
100    105    110

His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
115    120    125

His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
130    135    140

Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145    150    155    160

Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
165    170    175

Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
180    185    190

Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
195    200    205

Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
210    215    220

Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225    230    235    240

Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
245    250    255

Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
260    265    270

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Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp  
 275 280 285  
 Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp  
 290 295 300  
 Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser  
 305 310 315 320  
 Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys  
 325 330 335  
 Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe  
 340 345 350  
 Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser  
 355 360 365  
 Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp  
 370 375 380  
 Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg  
 385 390 395 400  
 Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu  
 405 410 415  
 Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe  
 420 425 430  
 Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile  
 435 440 445  
 Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp  
 450 455 460  
 Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu  
 465 470 475 480  
 Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr  
 485 490 495  
 Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser  
 500 505 510  
 Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys  
 515 520 525  
 Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln  
 530 535 540  
 Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr  
 545 550 555 560  
 Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp  
 565 570 575  
 Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly  
 580 585 590  
 Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp  
 595 600 605  
 Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr  
 610 615 620  
 Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala  
 625 630 635 640  
 His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr  
 645 650 655  
 Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp  
 660 665 670  
 Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe  
 675 680 685

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Ala	Asn	Arg	Asn	Phe	Met	Gln	Leu	Ile	His	Asp	Asp	Ser	Leu	Thr	Phe
	690					695					700				
Lys	Glu	Asp	Ile	Gln	Lys	Ala	Gln	Val	Ser	Gly	Gln	Gly	Asp	Ser	Leu
705					710					715					720
His	Glu	His	Ile	Ala	Asn	Leu	Ala	Gly	Ser	Pro	Ala	Ile	Lys	Lys	Gly
				725					730					735	
Ile	Leu	Gln	Thr	Val	Lys	Val	Val	Asp	Glu	Leu	Val	Lys	Val	Met	Gly
			740					745					750		
Arg	His	Lys	Pro	Glu	Asn	Ile	Val	Ile	Glu	Met	Ala	Arg	Glu	Asn	Gln
		755					760					765			
Thr	Thr	Gln	Lys	Gly	Gln	Lys	Asn	Ser	Arg	Glu	Arg	Met	Lys	Arg	Ile
	770					775					780				
Glu	Glu	Gly	Ile	Lys	Glu	Leu	Gly	Ser	Gln	Ile	Leu	Lys	Glu	His	Pro
785					790					795					800
Val	Glu	Asn	Thr	Gln	Leu	Gln	Asn	Glu	Lys	Leu	Tyr	Leu	Tyr	Tyr	Leu
				805					810					815	
Gln	Asn	Gly	Arg	Asp	Met	Tyr	Val	Asp	Gln	Glu	Leu	Asp	Ile	Asn	Arg
			820					825					830		
Leu	Ser	Asp	Tyr	Asp	Val	Asp	His	Ile	Val	Pro	Gln	Ser	Phe	Leu	Lys
		835					840					845			
Asp	Asp	Ser	Ile	Asp	Asn	Lys	Val	Leu	Thr	Arg	Ser	Asp	Lys	Asn	Arg
	850					855					860				
Gly	Lys	Ser	Asp	Asn	Val	Pro	Ser	Glu	Glu	Val	Val	Lys	Lys	Met	Lys
865					870					875					880
Asn	Tyr	Trp	Arg	Gln	Leu	Leu	Asn	Ala	Lys	Leu	Ile	Thr	Gln	Arg	Lys
				885					890					895	
Phe	Asp	Asn	Leu	Thr	Lys	Ala	Glu	Arg	Gly	Gly	Leu	Ser	Glu	Leu	Asp
			900					905					910		
Lys	Ala	Gly	Phe	Ile	Lys	Arg	Gln	Leu	Val	Glu	Thr	Arg	Gln	Ile	Thr
		915					920					925			
Lys	His	Val	Ala	Gln	Ile	Leu	Asp	Ser	Arg	Met	Asn	Thr	Lys	Tyr	Asp
	930					935					940				
Glu	Asn	Asp	Lys	Leu	Ile	Arg	Glu	Val	Lys	Val	Ile	Thr	Leu	Lys	Ser
945					950					955					960
Lys	Leu	Val	Ser	Asp	Phe	Arg	Lys	Asp	Phe	Gln	Phe	Tyr	Lys	Val	Arg
			965					970					975		
Glu	Ile	Asn	Asn	Tyr	His	His	Ala	His	Asp	Ala	Tyr	Leu	Asn	Ala	Val
			980					985					990		
Val	Gly	Thr	Ala	Leu	Ile	Lys	Lys	Tyr	Pro	Lys	Leu	Glu	Ser	Glu	Phe
		995					1000					1005			
Val	Tyr	Gly	Asp	Tyr	Lys	Val	Tyr	Asp	Val	Arg	Lys	Met	Ile	Ala	
	1010					1015					1020				
Lys	Ser	Glu	Gln	Glu	Ile	Gly	Lys	Ala	Thr	Ala	Lys	Tyr	Phe	Phe	
	1025					1030					1035				
Tyr	Ser	Asn	Ile	Met	Asn	Phe	Phe	Lys	Thr	Glu	Ile	Thr	Leu	Ala	
	1040					1045					1050				
Asn	Gly	Glu	Ile	Arg	Lys	Arg	Pro	Leu	Ile	Glu	Thr	Asn	Gly	Glu	
	1055					1060					1065				
Thr	Gly	Glu	Ile	Val	Trp	Asp	Lys	Gly	Arg	Asp	Phe	Ala	Thr	Val	
	1070					1075					1080				
Arg	Lys	Val	Leu	Ser	Met	Pro	Gln	Val	Asn	Ile	Val	Lys	Lys	Thr	
	1085					1090					1095				
Glu	Val	Gln	Thr	Gly	Gly	Phe	Ser	Lys	Glu	Ser	Ile	Leu	Pro	Lys	

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1100	1105	1110
Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro 1115	1120	1125
Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val 1130	1135	1140
Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys 1145	1150	1155
Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser 1160	1165	1170
Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys 1175	1180	1185
Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr Ser Leu 1190	1195	1200
Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly 1205	1210	1215
Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val 1220	1225	1230
Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser 1235	1240	1245
Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys 1250	1255	1260
His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys 1265	1270	1275
Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala 1280	1285	1290
Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn 1295	1300	1305
Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala 1310	1315	1320
Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser 1325	1330	1335
Thr Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr 1340	1345	1350
Gly Leu Tyr Glu Thr Arg Ile Asp Leu Ser Gln Leu Gly Gly Asp 1355	1360	1365

&lt;210&gt; SEQ ID NO 33

&lt;211&gt; LENGTH: 1053

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Staphylococcus aureus

&lt;400&gt; SEQUENCE: 33

Met Lys Arg Asn Tyr Ile Leu Gly Leu Asp Ile Gly Ile Thr Ser Val 1	5	10	15
Gly Tyr Gly Ile Ile Asp Tyr Glu Thr Arg Asp Val Ile Asp Ala Gly 20	25	30	
Val Arg Leu Phe Lys Glu Ala Asn Val Glu Asn Asn Glu Gly Arg Arg 35	40	45	
Ser Lys Arg Gly Ala Arg Arg Leu Lys Arg Arg Arg Arg His Arg Ile 50	55	60	
Gln Arg Val Lys Lys Leu Leu Phe Asp Tyr Asn Leu Leu Thr Asp His 65	70	75	80
Ser Glu Leu Ser Gly Ile Asn Pro Tyr Glu Ala Arg Val Lys Gly Leu 85	90	95	



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Ser Gln Lys Leu Ser Glu Glu Glu Phe Ser Ala Ala Leu Leu His Leu  
 100 105 110  
 Ala Lys Arg Arg Gly Val His Asn Val Asn Glu Val Glu Glu Asp Thr  
 115 120 125  
 Gly Asn Glu Leu Ser Thr Lys Glu Gln Ile Ser Arg Asn Ser Lys Ala  
 130 135 140  
 Leu Glu Glu Lys Tyr Val Ala Glu Leu Gln Leu Glu Arg Leu Lys Lys  
 145 150 155 160  
 Asp Gly Glu Val Arg Gly Ser Ile Asn Arg Phe Lys Thr Ser Asp Tyr  
 165 170 175  
 Val Lys Glu Ala Lys Gln Leu Leu Lys Val Gln Lys Ala Tyr His Gln  
 180 185 190  
 Leu Asp Gln Ser Phe Ile Asp Thr Tyr Ile Asp Leu Leu Glu Thr Arg  
 195 200 205  
 Arg Thr Tyr Tyr Glu Gly Pro Gly Glu Gly Ser Pro Phe Gly Trp Lys  
 210 215 220  
 Asp Ile Lys Glu Trp Tyr Glu Met Leu Met Gly His Cys Thr Tyr Phe  
 225 230 235 240  
 Pro Glu Glu Leu Arg Ser Val Lys Tyr Ala Tyr Asn Ala Asp Leu Tyr  
 245 250 255  
 Asn Ala Leu Asn Asp Leu Asn Asn Leu Val Ile Thr Arg Asp Glu Asn  
 260 265 270  
 Glu Lys Leu Glu Tyr Tyr Glu Lys Phe Gln Ile Ile Glu Asn Val Phe  
 275 280 285  
 Lys Gln Lys Lys Lys Pro Thr Leu Lys Gln Ile Ala Lys Glu Ile Leu  
 290 295 300  
 Val Asn Glu Glu Asp Ile Lys Gly Tyr Arg Val Thr Ser Thr Gly Lys  
 305 310 315 320  
 Pro Glu Phe Thr Asn Leu Lys Val Tyr His Asp Ile Lys Asp Ile Thr  
 325 330 335  
 Ala Arg Lys Glu Ile Ile Glu Asn Ala Glu Leu Leu Asp Gln Ile Ala  
 340 345 350  
 Lys Ile Leu Thr Ile Tyr Gln Ser Ser Glu Asp Ile Gln Glu Glu Leu  
 355 360 365  
 Thr Asn Leu Asn Ser Glu Leu Thr Gln Glu Glu Ile Glu Gln Ile Ser  
 370 375 380  
 Asn Leu Lys Gly Tyr Thr Gly Thr His Asn Leu Ser Leu Lys Ala Ile  
 385 390 395 400  
 Asn Leu Ile Leu Asp Glu Leu Trp His Thr Asn Asp Asn Gln Ile Ala  
 405 410 415  
 Ile Phe Asn Arg Leu Lys Leu Val Pro Lys Lys Val Asp Leu Ser Gln  
 420 425 430  
 Gln Lys Glu Ile Pro Thr Thr Leu Val Asp Asp Phe Ile Leu Ser Pro  
 435 440 445  
 Val Val Lys Arg Ser Phe Ile Gln Ser Ile Lys Val Ile Asn Ala Ile  
 450 455 460  
 Ile Lys Lys Tyr Gly Leu Pro Asn Asp Ile Ile Ile Glu Leu Ala Arg  
 465 470 475 480  
 Glu Lys Asn Ser Lys Asp Ala Gln Lys Met Ile Asn Glu Met Gln Lys  
 485 490 495  
 Arg Asn Arg Gln Thr Asn Glu Arg Ile Glu Glu Ile Ile Arg Thr Thr  
 500 505 510  
 Gly Lys Glu Asn Ala Lys Tyr Leu Ile Glu Lys Ile Lys Leu His Asp

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515					520					525					
Met	Gln	Glu	Gly	Lys	Cys	Leu	Tyr	Ser	Leu	Glu	Ala	Ile	Pro	Leu	Glu
	530					535					540				
Asp	Leu	Leu	Asn	Asn	Pro	Phe	Asn	Tyr	Glu	Val	Asp	His	Ile	Ile	Pro
	545					550					555				560
Arg	Ser	Val	Ser	Phe	Asp	Asn	Ser	Phe	Asn	Asn	Lys	Val	Leu	Val	Lys
				565					570					575	
Gln	Glu	Glu	Asn	Ser	Lys	Lys	Gly	Asn	Arg	Thr	Pro	Phe	Gln	Tyr	Leu
			580					585					590		
Ser	Ser	Ser	Asp	Ser	Lys	Ile	Ser	Tyr	Glu	Thr	Phe	Lys	Lys	His	Ile
		595					600					605			
Leu	Asn	Leu	Ala	Lys	Gly	Lys	Gly	Arg	Ile	Ser	Lys	Thr	Lys	Lys	Glu
	610					615					620				
Tyr	Leu	Leu	Glu	Glu	Arg	Asp	Ile	Asn	Arg	Phe	Ser	Val	Gln	Lys	Asp
	625					630					635				640
Phe	Ile	Asn	Arg	Asn	Leu	Val	Asp	Thr	Arg	Tyr	Ala	Thr	Arg	Gly	Leu
				645					650					655	
Met	Asn	Leu	Leu	Arg	Ser	Tyr	Phe	Arg	Val	Asn	Asn	Leu	Asp	Val	Lys
			660					665					670		
Val	Lys	Ser	Ile	Asn	Gly	Gly	Phe	Thr	Ser	Phe	Leu	Arg	Arg	Lys	Trp
		675					680					685			
Lys	Phe	Lys	Lys	Glu	Arg	Asn	Lys	Gly	Tyr	Lys	His	His	Ala	Glu	Asp
	690					695					700				
Ala	Leu	Ile	Ile	Ala	Asn	Ala	Asp	Phe	Ile	Phe	Lys	Glu	Trp	Lys	Lys
	705					710					715				720
Leu	Asp	Lys	Ala	Lys	Lys	Val	Met	Glu	Asn	Gln	Met	Phe	Glu	Glu	Lys
				725					730					735	
Gln	Ala	Glu	Ser	Met	Pro	Glu	Ile	Glu	Thr	Glu	Gln	Glu	Tyr	Lys	Glu
			740					745					750		
Ile	Phe	Ile	Thr	Pro	His	Gln	Ile	Lys	His	Ile	Lys	Asp	Phe	Lys	Asp
		755					760					765			
Tyr	Lys	Tyr	Ser	His	Arg	Val	Asp	Lys	Lys	Pro	Asn	Arg	Glu	Leu	Ile
	770						775				780				
Asn	Asp	Thr	Leu	Tyr	Ser	Thr	Arg	Lys	Asp	Asp	Lys	Gly	Asn	Thr	Leu
	785					790					795				800
Ile	Val	Asn	Asn	Leu	Asn	Gly	Leu	Tyr	Asp	Lys	Asp	Asn	Asp	Lys	Leu
				805					810					815	
Lys	Lys	Leu	Ile	Asn	Lys	Ser	Pro	Glu	Lys	Leu	Leu	Met	Tyr	His	His
			820					825					830		
Asp	Pro	Gln	Thr	Tyr	Gln	Lys	Leu	Lys	Leu	Ile	Met	Glu	Gln	Tyr	Gly
		835					840					845			
Asp	Glu	Lys	Asn	Pro	Leu	Tyr	Lys	Tyr	Tyr	Glu	Glu	Thr	Gly	Asn	Tyr
	850					855					860				
Leu	Thr	Lys	Tyr	Ser	Lys	Lys	Asp	Asn	Gly	Pro	Val	Ile	Lys	Lys	Ile
	865					870					875				880
Lys	Tyr	Tyr	Gly	Asn	Lys	Leu	Asn	Ala	His	Leu	Asp	Ile	Thr	Asp	Asp
				885					890					895	
Tyr	Pro	Asn	Ser	Arg	Asn	Lys	Val	Val	Lys	Leu	Ser	Leu	Lys	Pro	Tyr
			900					905					910		
Arg	Phe	Asp	Val	Tyr	Leu	Asp	Asn	Gly	Val	Tyr	Lys	Phe	Val	Thr	Val
		915					920					925			
Lys	Asn	Leu	Asp	Val	Ile	Lys	Lys	Glu	Asn	Tyr	Tyr	Glu	Val	Asn	Ser
	930					935					940				

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Lys Cys Tyr Glu Glu Ala Lys Lys Leu Lys Lys Ile Ser Asn Gln Ala  
 945 950 955 960  
 Glu Phe Ile Ala Ser Phe Tyr Asn Asn Asp Leu Ile Lys Ile Asn Gly  
 965 970 975  
 Glu Leu Tyr Arg Val Ile Gly Val Asn Asn Asp Leu Leu Asn Arg Ile  
 980 985 990  
 Glu Val Asn Met Ile Asp Ile Thr Tyr Arg Glu Tyr Leu Glu Asn Met  
 995 1000 1005  
 Asn Asp Lys Arg Pro Pro Arg Ile Ile Lys Thr Ile Ala Ser Lys  
 1010 1015 1020  
 Thr Gln Ser Ile Lys Lys Tyr Ser Thr Asp Ile Leu Gly Asn Leu  
 1025 1030 1035  
 Tyr Glu Val Lys Ser Lys Lys His Pro Gln Ile Ile Lys Lys Gly  
 1040 1045 1050

<210> SEQ ID NO 34  
 <211> LENGTH: 1300  
 <212> TYPE: PRT  
 <213> ORGANISM: Francisella tularensis

<400> SEQUENCE: 34

Met Ser Ile Tyr Gln Glu Phe Val Asn Lys Tyr Ser Leu Ser Lys Thr  
 1 5 10 15  
 Leu Arg Phe Glu Leu Ile Pro Gln Gly Lys Thr Leu Glu Asn Ile Lys  
 20 25 30  
 Ala Arg Gly Leu Ile Leu Asp Asp Glu Lys Arg Ala Lys Asp Tyr Lys  
 35 40 45  
 Lys Ala Lys Gln Ile Ile Asp Lys Tyr His Gln Phe Phe Ile Glu Glu  
 50 55 60  
 Ile Leu Ser Ser Val Cys Ile Ser Glu Asp Leu Leu Gln Asn Tyr Ser  
 65 70 75 80  
 Asp Val Tyr Phe Lys Leu Lys Lys Ser Asp Asp Asp Asn Leu Gln Lys  
 85 90 95  
 Asp Phe Lys Ser Ala Lys Asp Thr Ile Lys Lys Gln Ile Ser Glu Tyr  
 100 105 110  
 Ile Lys Asp Ser Glu Lys Phe Lys Asn Leu Phe Asn Gln Asn Leu Ile  
 115 120 125  
 Asp Ala Lys Lys Gly Gln Glu Ser Asp Leu Ile Leu Trp Leu Lys Gln  
 130 135 140  
 Ser Lys Asp Asn Gly Ile Glu Leu Phe Lys Ala Asn Ser Asp Ile Thr  
 145 150 155 160  
 Asp Ile Asp Glu Ala Leu Glu Ile Ile Lys Ser Phe Lys Gly Trp Thr  
 165 170 175  
 Thr Tyr Phe Lys Gly Phe His Glu Asn Arg Lys Asn Val Tyr Ser Ser  
 180 185 190  
 Asn Asp Ile Pro Thr Ser Ile Ile Tyr Arg Ile Val Asp Asp Asn Leu  
 195 200 205  
 Pro Lys Phe Leu Glu Asn Lys Ala Lys Tyr Glu Ser Leu Lys Asp Lys  
 210 215 220  
 Ala Pro Glu Ala Ile Asn Tyr Glu Gln Ile Lys Lys Asp Leu Ala Glu  
 225 230 235 240  
 Glu Leu Thr Phe Asp Ile Asp Tyr Lys Thr Ser Glu Val Asn Gln Arg  
 245 250 255  
 Val Phe Ser Leu Asp Glu Val Phe Glu Ile Ala Asn Phe Asn Asn Tyr

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260			265			270									
Leu	Asn	Gln	Ser	Gly	Ile	Thr	Lys	Phe	Asn	Thr	Ile	Ile	Gly	Gly	Lys
	275						280					285			
Phe	Val	Asn	Gly	Glu	Asn	Thr	Lys	Arg	Lys	Gly	Ile	Asn	Glu	Tyr	Ile
	290						295				300				
Asn	Leu	Tyr	Ser	Gln	Gln	Ile	Asn	Asp	Lys	Thr	Leu	Lys	Lys	Tyr	Lys
305					310					315					320
Met	Ser	Val	Leu	Phe	Lys	Gln	Ile	Leu	Ser	Asp	Thr	Glu	Ser	Lys	Ser
				325					330					335	
Phe	Val	Ile	Asp	Lys	Leu	Glu	Asp	Asp	Ser	Asp	Val	Val	Thr	Thr	Met
			340					345					350		
Gln	Ser	Phe	Tyr	Glu	Gln	Ile	Ala	Ala	Phe	Lys	Thr	Val	Glu	Glu	Lys
		355					360					365			
Ser	Ile	Lys	Glu	Thr	Leu	Ser	Leu	Leu	Phe	Asp	Asp	Leu	Lys	Ala	Gln
	370					375					380				
Lys	Leu	Asp	Leu	Ser	Lys	Ile	Tyr	Phe	Lys	Asn	Asp	Lys	Ser	Leu	Thr
385					390					395					400
Asp	Leu	Ser	Gln	Gln	Val	Phe	Asp	Asp	Tyr	Ser	Val	Ile	Gly	Thr	Ala
				405					410					415	
Val	Leu	Glu	Tyr	Ile	Thr	Gln	Gln	Ile	Ala	Pro	Lys	Asn	Leu	Asp	Asn
			420					425					430		
Pro	Ser	Lys	Lys	Glu	Gln	Glu	Leu	Ile	Ala	Lys	Lys	Thr	Glu	Lys	Ala
		435					440					445			
Lys	Tyr	Leu	Ser	Leu	Glu	Thr	Ile	Lys	Leu	Ala	Leu	Glu	Glu	Phe	Asn
	450					455					460				
Lys	His	Arg	Asp	Ile	Asp	Lys	Gln	Cys	Arg	Phe	Glu	Glu	Ile	Leu	Ala
465					470					475					480
Asn	Phe	Ala	Ala	Ile	Pro	Met	Ile	Phe	Asp	Glu	Ile	Ala	Gln	Asn	Lys
				485					490					495	
Asp	Asn	Leu	Ala	Gln	Ile	Ser	Ile	Lys	Tyr	Gln	Asn	Gln	Gly	Lys	Lys
		500						505					510		
Asp	Leu	Leu	Gln	Ala	Ser	Ala	Glu	Asp	Asp	Val	Lys	Ala	Ile	Lys	Asp
		515					520					525			
Leu	Leu	Asp	Gln	Thr	Asn	Asn	Leu	Leu	His	Lys	Leu	Lys	Ile	Phe	His
	530					535					540				
Ile	Ser	Gln	Ser	Glu	Asp	Lys	Ala	Asn	Ile	Leu	Asp	Lys	Asp	Glu	His
545					550					555					560
Phe	Tyr	Leu	Val	Phe	Glu	Glu	Cys	Tyr	Phe	Glu	Leu	Ala	Asn	Ile	Val
				565					570					575	
Pro	Leu	Tyr	Asn	Lys	Ile	Arg	Asn	Tyr	Ile	Thr	Gln	Lys	Pro	Tyr	Ser
			580					585					590		
Asp	Glu	Lys	Phe	Lys	Leu	Asn	Phe	Glu	Asn	Ser	Thr	Leu	Ala	Asn	Gly
		595					600					605			
Trp	Asp	Lys	Asn	Lys	Glu	Pro	Asp	Asn	Thr	Ala	Ile	Leu	Phe	Ile	Lys
	610					615					620				
Asp	Asp	Lys	Tyr	Tyr	Leu	Gly	Val	Met	Asn	Lys	Lys	Asn	Asn	Lys	Ile
625					630					635					640
Phe	Asp	Asp	Lys	Ala	Ile	Lys	Glu	Asn	Lys	Gly	Glu	Gly	Tyr	Lys	Lys
				645					650					655	
Ile	Val	Tyr	Lys	Leu	Leu	Pro	Gly	Ala	Asn	Lys	Met	Leu	Pro	Lys	Val
			660					665					670		
Phe	Phe	Ser	Ala	Lys	Ser	Ile	Lys	Phe	Tyr	Asn	Pro	Ser	Glu	Asp	Ile
		675					680						685		

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Leu Arg Ile Arg Asn His Ser Thr His Thr Lys Asn Gly Ser Pro Gln  
 690 695 700

Lys Gly Tyr Glu Lys Phe Glu Phe Asn Ile Glu Asp Cys Arg Lys Phe  
 705 710 715 720

Ile Asp Phe Tyr Lys Gln Ser Ile Ser Lys His Pro Glu Trp Lys Asp  
 725 730 735

Phe Gly Phe Arg Phe Ser Asp Thr Gln Arg Tyr Asn Ser Ile Asp Glu  
 740 745 750

Phe Tyr Arg Glu Val Glu Asn Gln Gly Tyr Lys Leu Thr Phe Glu Asn  
 755 760 765

Ile Ser Glu Ser Tyr Ile Asp Ser Val Val Asn Gln Gly Lys Leu Tyr  
 770 775 780

Leu Phe Gln Ile Tyr Asn Lys Asp Phe Ser Ala Tyr Ser Lys Gly Arg  
 785 790 795 800

Pro Asn Leu His Thr Leu Tyr Trp Lys Ala Leu Phe Asp Glu Arg Asn  
 805 810 815

Leu Gln Asp Val Val Tyr Lys Leu Asn Gly Glu Ala Glu Leu Phe Tyr  
 820 825 830

Arg Lys Gln Ser Ile Pro Lys Lys Ile Thr His Pro Ala Lys Glu Ala  
 835 840 845

Ile Ala Asn Lys Asn Lys Asp Asn Pro Lys Lys Glu Ser Val Phe Glu  
 850 855 860

Tyr Asp Leu Ile Lys Asp Lys Arg Phe Thr Glu Asp Lys Phe Phe Phe  
 865 870 875 880

His Cys Pro Ile Thr Ile Asn Phe Lys Ser Ser Gly Ala Asn Lys Phe  
 885 890 895

Asn Asp Glu Ile Asn Leu Leu Leu Lys Glu Lys Ala Asn Asp Val His  
 900 905 910

Ile Leu Ser Ile Asp Arg Gly Glu Arg His Leu Ala Tyr Tyr Thr Leu  
 915 920 925

Val Asp Gly Lys Gly Asn Ile Ile Lys Gln Asp Thr Phe Asn Ile Ile  
 930 935 940

Gly Asn Asp Arg Met Lys Thr Asn Tyr His Asp Lys Leu Ala Ala Ile  
 945 950 955 960

Glu Lys Asp Arg Asp Ser Ala Arg Lys Asp Trp Lys Lys Ile Asn Asn  
 965 970 975

Ile Lys Glu Met Lys Glu Gly Tyr Leu Ser Gln Val Val His Glu Ile  
 980 985 990

Ala Lys Leu Val Ile Glu Tyr Asn Ala Ile Val Val Phe Glu Asp Leu  
 995 1000 1005

Asn Phe Gly Phe Lys Arg Gly Arg Phe Lys Val Glu Lys Gln Val  
 1010 1015 1020

Tyr Gln Lys Leu Glu Lys Met Leu Ile Glu Lys Leu Asn Tyr Leu  
 1025 1030 1035

Val Phe Lys Asp Asn Glu Phe Asp Lys Thr Gly Gly Val Leu Arg  
 1040 1045 1050

Ala Tyr Gln Leu Thr Ala Pro Phe Glu Thr Phe Lys Lys Met Gly  
 1055 1060 1065

Lys Gln Thr Gly Ile Ile Tyr Tyr Val Pro Ala Gly Phe Thr Ser  
 1070 1075 1080

Lys Ile Cys Pro Val Thr Gly Phe Val Asn Gln Leu Tyr Pro Lys  
 1085 1090 1095

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Tyr Glu Ser Val Ser Lys Ser Gln Glu Phe Phe Ser Lys Phe Asp  
 1100 1105 1110  
 Lys Ile Cys Tyr Asn Leu Asp Lys Gly Tyr Phe Glu Phe Ser Phe  
 1115 1120 1125  
 Asp Tyr Lys Asn Phe Gly Asp Lys Ala Ala Lys Gly Lys Trp Thr  
 1130 1135 1140  
 Ile Ala Ser Phe Gly Ser Arg Leu Ile Asn Phe Arg Asn Ser Asp  
 1145 1150 1155  
 Lys Asn His Asn Trp Asp Thr Arg Glu Val Tyr Pro Thr Lys Glu  
 1160 1165 1170  
 Leu Glu Lys Leu Leu Lys Asp Tyr Ser Ile Glu Tyr Gly His Gly  
 1175 1180 1185  
 Glu Cys Ile Lys Ala Ala Ile Cys Gly Glu Ser Asp Lys Lys Phe  
 1190 1195 1200  
 Phe Ala Lys Leu Thr Ser Val Leu Asn Thr Ile Leu Gln Met Arg  
 1205 1210 1215  
 Asn Ser Lys Thr Gly Thr Glu Leu Asp Tyr Leu Ile Ser Pro Val  
 1220 1225 1230  
 Ala Asp Val Asn Gly Asn Phe Phe Asp Ser Arg Gln Ala Pro Lys  
 1235 1240 1245  
 Asn Met Pro Gln Asp Ala Asp Ala Asn Gly Ala Tyr His Ile Gly  
 1250 1255 1260  
 Leu Lys Gly Leu Met Leu Leu Gly Arg Ile Lys Asn Asn Gln Glu  
 1265 1270 1275  
 Gly Lys Lys Leu Asn Leu Val Ile Lys Asn Glu Glu Tyr Phe Glu  
 1280 1285 1290  
 Phe Val Gln Asn Arg Asn Asn  
 1295 1300

&lt;210&gt; SEQ ID NO 35

&lt;211&gt; LENGTH: 297

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Adeno-associated virus-1

&lt;400&gt; SEQUENCE: 35

Thr Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala  
 1 5 10 15  
 His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr  
 20 25 30  
 Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn  
 35 40 45  
 Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln  
 50 55 60  
 Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser  
 65 70 75 80  
 Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala  
 85 90 95  
 Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr  
 100 105 110  
 Ala Met Ala Ser His Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser  
 115 120 125  
 Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala  
 130 135 140  
 Leu Asp Asn Val Met Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn  
 145 150 155 160

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Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Phe Lys Asp  
 165 170 175

Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly Lys  
 180 185 190

Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile Thr  
 195 200 205

Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg Phe  
 210 215 220

Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala Thr  
 225 230 235 240

Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln Asp  
 245 250 255

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr  
 260 265 270

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys  
 275 280 285

Asn Pro Pro Pro Gln Ile Leu Ile Lys  
 290 295

<210> SEQ ID NO 36  
 <211> LENGTH: 240  
 <212> TYPE: PRT  
 <213> ORGANISM: Adeno-associated virus-6

<400> SEQUENCE: 36

Thr Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala  
 1 5 10 15

His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr  
 20 25 30

Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn  
 35 40 45

Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln  
 50 55 60

Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser  
 65 70 75 80

Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala  
 85 90 95

Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr  
 100 105 110

Ala Met Ala Ser His Lys Asp Asp Lys Asp Lys Phe Phe Pro Met Ser  
 115 120 125

Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala  
 130 135 140

Leu Asp Asn Val Met Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn  
 145 150 155 160

Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Leu Gln Ser  
 165 170 175

Ser Ser Thr Asp Pro Ala Thr Gly Asp Val His Val Met Gly Ala Leu  
 180 185 190

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile  
 195 200 205

Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu  
 210 215 220

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys

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225                          230                          235                          240

<210> SEQ ID NO 37  
<211> LENGTH: 240  
<212> TYPE: PRT  
<213> ORGANISM: Adeno-associated virus-3

<400> SEQUENCE: 37

Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His  
1                          5                          10                          15

Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu  
                        20                          25                          30

Tyr Tyr Leu Asn Arg Thr Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln  
                        35                          40                          45

Ser Arg Leu Leu Phe Ser Gln Ala Gly Pro Gln Ser Met Ser Leu Gln  
50                          55                          60

Ala Arg Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser  
65                          70                          75                          80

Lys Thr Ala Asn Asp Asn Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala  
                        85                          90                          95

Ser Lys Tyr His Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro  
                        100                          105                          110

Ala Met Ala Ser His Lys Asp Asp Glu Glu Lys Phe Phe Pro Met His  
                        115                          120                          125

Gly Asn Leu Ile Phe Gly Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu  
130                          135                          140

Leu Asp Asn Val Met Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn  
145                          150                          155                          160

Pro Val Ala Thr Glu Gln Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser  
                        165                          170                          175

Ser Asn Thr Ala Pro Thr Thr Gly Thr Val Asn His Gln Gly Ala Leu  
                        180                          185                          190

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile  
                        195                          200                          205

Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu  
210                          215                          220

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Met Ile Lys  
225                          230                          235                          240

<210> SEQ ID NO 38  
<211> LENGTH: 240  
<212> TYPE: PRT  
<213> ORGANISM: Adeno-associated virus-2

<400> SEQUENCE: 38

Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His  
1                          5                          10                          15

Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu  
                        20                          25                          30

Tyr Tyr Leu Ser Arg Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser  
                        35                          40                          45

Arg Leu Gln Phe Ser Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser  
50                          55                          60

Arg Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys  
65                          70                          75                          80

Thr Ser Ala Asp Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr



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85					90					95					
Lys	Tyr	His	Leu	Asn	Gly	Arg	Asp	Ser	Leu	Val	Asn	Pro	Gly	Pro	Ala
			100					105					110		
Met	Ala	Ser	His	Lys	Asp	Asp	Glu	Glu	Lys	Phe	Phe	Pro	Gln	Ser	Gly
		115					120					125			
Val	Leu	Ile	Phe	Gly	Lys	Gln	Gly	Ser	Glu	Lys	Thr	Asn	Val	Asp	Ile
	130					135					140				
Glu	Lys	Val	Met	Ile	Thr	Asp	Glu	Glu	Glu	Ile	Arg	Thr	Thr	Asn	Pro
145					150					155					160
Val	Ala	Thr	Glu	Gln	Tyr	Gly	Ser	Val	Ser	Thr	Asn	Leu	Gln	Arg	Gly
				165					170					175	
Asn	Arg	Gln	Ala	Ala	Thr	Ala	Asp	Val	Asn	Thr	Gln	Gly	Val	Leu	Pro
			180					185					190		
Gly	Met	Val	Trp	Gln	Asp	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp
		195					200					205			
Ala	Lys	Ile	Pro	His	Thr	Asp	Gly	His	Phe	His	Pro	Ser	Pro	Leu	Met
	210					215					220				
Gly	Gly	Phe	Gly	Leu	Lys	His	Pro	Pro	Pro	Gln	Ile	Leu	Ile	Lys	Asn
225					230					235					240

&lt;210&gt; SEQ ID NO 39

&lt;211&gt; LENGTH: 243

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Adeno-associated virus-8

&lt;400&gt; SEQUENCE: 39

Asn	Phe	Gln	Phe	Thr	Tyr	Thr	Phe	Glu	Asp	Val	Pro	Phe	His	Ser	Ser
1				5					10					15	
Tyr	Ala	His	Ser	Gln	Ser	Leu	Asp	Arg	Leu	Met	Asn	Pro	Leu	Ile	Asp
			20					25					30		
Gln	Tyr	Leu	Tyr	Tyr	Leu	Ser	Arg	Thr	Gln	Thr	Thr	Gly	Gly	Thr	Ala
		35					40					45			
Asn	Thr	Gln	Thr	Leu	Gly	Phe	Ser	Gln	Gly	Gly	Pro	Asn	Thr	Met	Ala
	50					55					60				
Asn	Gln	Ala	Lys	Asn	Trp	Leu	Pro	Gly	Pro	Cys	Tyr	Arg	Gln	Gln	Arg
65					70					75					80
Val	Ser	Thr	Thr	Thr	Gly	Gln	Asn	Asn	Asn	Ser	Asn	Phe	Ala	Trp	Thr
				85					90					95	
Ala	Gly	Thr	Lys	Tyr	His	Leu	Asn	Gly	Arg	Asn	Ser	Leu	Ala	Asn	Pro
			100					105					110		
Gly	Ile	Ala	Met	Ala	Thr	His	Lys	Asp	Asp	Glu	Glu	Arg	Phe	Phe	Pro
		115					120					125			
Ser	Asn	Gly	Ile	Leu	Ile	Phe	Gly	Lys	Gln	Asn	Ala	Ala	Arg	Asp	Asn
	130					135					140				
Ala	Asp	Tyr	Ser	Asp	Val	Met	Leu	Thr	Ser	Glu	Glu	Glu	Ile	Lys	Thr
145					150					155					160
Thr	Asn	Pro	Val	Ala	Thr	Glu	Glu	Tyr	Gly	Ile	Val	Ala	Asp	Asn	Leu
				165					170					175	
Gln	Gln	Gln	Asn	Thr	Ala	Pro	Gln	Ile	Gly	Thr	Val	Asn	Ser	Gln	Gly
			180					185					190		
Ala	Leu	Pro	Gly	Met	Val	Trp	Gln	Asn	Arg	Asp	Val	Tyr	Leu	Gln	Gly
		195					200					205			
Pro	Ile	Trp	Ala	Lys	Ile	Pro	His	Thr	Asp	Gly	Asn	Phe	His	Pro	Ser
	210						215				220				

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Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu  
225 230 235 240

Ile Lys Asn

<210> SEQ ID NO 40  
 <211> LENGTH: 243  
 <212> TYPE: PRT  
 <213> ORGANISM: Adeno-associated virus-8.1

&lt;400&gt; SEQUENCE: 40

Asn Phe Gln Phe Thr Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser  
1 5 10 15

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp  
20 25 30

Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala  
35 40 45

Asn Thr Gln Thr Leu Gly Phe Ser Gln Gly Gly Pro Asn Thr Met Ala  
50 55 60

Asn Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg  
65 70 75 80

Val Ser Thr Thr Thr Gly Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr  
85 90 95

Ala Gly Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro  
100 105 110

Gly Ile Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg Phe Phe Pro  
115 120 125

Ser Asn Gly Ile Leu Ile Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn  
130 135 140

Ala Asp Tyr Ser Asp Val Met Leu Thr Ser Glu Glu Glu Ile Lys Thr  
145 150 155 160

Thr Asn Pro Val Ala Thr Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu  
165 170 175

Gln Gly Gln Arg Gln Ala Ala Gln Ile Gly Thr Val Asn Ser Gln Gly  
180 185 190

Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly  
195 200 205

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser  
210 215 220

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu  
225 230 235 240

Ile Lys Asn

<210> SEQ ID NO 41  
 <211> LENGTH: 241  
 <212> TYPE: PRT  
 <213> ORGANISM: Adeno-associated virus-8 Rh8

&lt;400&gt; SEQUENCE: 41

Phe Gln Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr  
1 5 10 15

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln  
20 25 30

Tyr Leu Tyr Tyr Leu Val Arg Thr Gln Thr Thr Gly Thr Gly Gly Thr  
35 40 45

Gln Thr Leu Ala Phe Ser Gln Ala Gly Pro Ser Ser Met Ala Asn Gln  
50 55 60

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Ala Arg Asn Trp Val Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser  
65 70 75 80

Thr Thr Thr Asn Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala  
85 90 95

Ala Lys Phe Lys Leu Asn Gly Arg Asp Ser Leu Met Asn Pro Gly Val  
100 105 110

Ala Met Ala Ser His Lys Asp Asp Asp Arg Phe Phe Pro Ser Ser  
115 120 125

Gly Val Leu Ile Phe Gly Lys Gln Gly Ala Gly Asn Asp Gly Val Asp  
130 135 140

Tyr Ser Gln Val Leu Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn  
145 150 155 160

Pro Val Ala Thr Glu Glu Tyr Gly Ala Val Ala Ile Asn Asn Gln Ala  
165 170 175

Ala Asn Thr Gln Ala Gln Thr Gly Leu Val His Asn Gln Gly Val Ile  
180 185 190

Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile  
195 200 205

Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu  
210 215 220

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys  
225 230 235 240

Asn

&lt;210&gt; SEQ ID NO 42

&lt;211&gt; LENGTH: 243

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Adeno-associated virus-10

&lt;400&gt; SEQUENCE: 42

Asn Phe Glu Phe Ser Tyr Thr Phe Glu Asp Val Pro Phe His Ser Ser  
1 5 10 15

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp  
20 25 30

Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln  
35 40 45

Gly Thr Gln Gln Leu Leu Phe Ser Gln Ala Gly Pro Ala Asn Met Ser  
50 55 60

Ala Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg  
65 70 75 80

Val Ser Thr Thr Leu Ser Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr  
85 90 95

Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp Ser Leu Val Asn Pro  
100 105 110

Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Glu Arg Phe Phe Pro  
115 120 125

Ser Ser Gly Val Leu Met Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn  
130 135 140

Val Asp Tyr Ser Ser Val Met Leu Thr Ser Glu Glu Glu Ile Lys Thr  
145 150 155 160

Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly Val Val Ala Asp Asn Leu  
165 170 175

Gln Gln Ala Asn Thr Gly Pro Ile Val Gly Asn Val Asn Ser Gln Gly  
180 185 190

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Ala Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly  
 195 200 205

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser  
 210 215 220

Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu  
 225 230 235 240

Ile Lys Asn

<210> SEQ ID NO 43  
 <211> LENGTH: 242  
 <212> TYPE: PRT  
 <213> ORGANISM: Adeno-associated virus-7

<400> SEQUENCE: 43

Phe Glu Phe Ser Tyr Ser Phe Glu Asp Val Pro Phe His Ser Ser Tyr  
 1 5 10 15

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln  
 20 25 30

Tyr Leu Tyr Tyr Leu Ala Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala  
 35 40 45

Gly Asn Arg Glu Leu Gln Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala  
 50 55 60

Glu Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg  
 65 70 75 80

Val Ser Lys Thr Leu Asp Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr  
 85 90 95

Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asn Ser Leu Val Asn Pro  
 100 105 110

Gly Val Ala Met Ala Thr His Lys Asp Asp Glu Asp Arg Phe Phe Pro  
 115 120 125

Ser Ser Gly Val Leu Ile Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr  
 130 135 140

Thr Leu Glu Asn Val Leu Met Thr Asn Glu Glu Glu Ile Arg Pro Thr  
 145 150 155 160

Asn Pro Val Ala Thr Glu Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln  
 165 170 175

Ala Ala Asn Thr Ala Ala Gln Thr Gln Val Val Asn Asn Gln Gly Ala  
 180 185 190

Leu Pro Gly Met Val Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro  
 195 200 205

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro  
 210 215 220

Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile  
 225 230 235 240

Lys Asn

<210> SEQ ID NO 44  
 <211> LENGTH: 240  
 <212> TYPE: PRT  
 <213> ORGANISM: Adeno-associated virus-9

<400> SEQUENCE: 44

Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser Tyr  
 1 5 10 15

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln

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20					25					30					
Tyr	Leu	Tyr	Tyr	Leu	Ser	Lys	Thr	Ile	Asn	Gly	Ser	Gly	Gln	Asn	Gln
	35						40					45			
Gln	Thr	Leu	Lys	Phe	Ser	Val	Ala	Gly	Pro	Ser	Asn	Met	Ala	Val	Gln
	50					55					60				
Gly	Arg	Asn	Tyr	Ile	Pro	Gly	Pro	Ser	Tyr	Arg	Gln	Gln	Arg	Val	Ser
65					70					75					80
Thr	Thr	Val	Thr	Gln	Asn	Asn	Asn	Ser	Glu	Phe	Ala	Trp	Pro	Gly	Ala
				85					90					95	
Ser	Ser	Trp	Ala	Leu	Asn	Gly	Arg	Asn	Ser	Leu	Met	Asn	Pro	Gly	Pro
			100					105					110		
Ala	Met	Ala	Ser	His	Lys	Glu	Gly	Glu	Asp	Arg	Phe	Phe	Pro	Leu	Ser
		115					120					125			
Gly	Ser	Leu	Ile	Phe	Gly	Lys	Gln	Gly	Thr	Gly	Arg	Asp	Asn	Val	Asp
	130					135					140				
Ala	Asp	Lys	Val	Met	Ile	Thr	Asn	Glu	Glu	Glu	Ile	Lys	Thr	Thr	Asn
145						150					155				160
Pro	Val	Ala	Thr	Glu	Ser	Tyr	Gly	Gln	Val	Ala	Thr	Asn	His	Gln	Ser
				165					170					175	
Ala	Gln	Ala	Gln	Ala	Gln	Thr	Gly	Trp	Val	Gln	Asn	Gln	Gly	Ile	Leu
			180					185					190		
Pro	Gly	Met	Val	Trp	Gln	Asp	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile
		195					200					205			
Trp	Ala	Lys	Ile	Pro	His	Thr	Asp	Gly	Asn	Phe	His	Pro	Ser	Pro	Leu
	210					215					220				
Met	Gly	Gly	Phe	Gly	Met	Lys	His	Pro	Pro	Pro	Gln	Ile	Leu	Ile	Lys
225					230					235					240

&lt;210&gt; SEQ ID NO 45

&lt;211&gt; LENGTH: 240

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Adeno-associated virus-9.1

&lt;400&gt; SEQUENCE: 45

Phe	Gln	Phe	Ser	Tyr	Glu	Phe	Glu	Asn	Val	Pro	Phe	His	Ser	Ser	Tyr
1				5					10					15	
Ala	His	Ser	Gln	Ser	Leu	Asp	Arg	Leu	Met	Asn	Pro	Leu	Ile	Asp	Gln
			20					25					30		
Tyr	Leu	Tyr	Tyr	Leu	Ser	Lys	Thr	Ile	Asn	Gly	Ser	Gly	Gln	Asn	Gln
	35						40					45			
Gln	Thr	Leu	Lys	Phe	Ser	Val	Ala	Gly	Pro	Ser	Asn	Met	Ala	Val	Gln
	50					55					60				
Gly	Arg	Asn	Tyr	Ile	Pro	Gly	Pro	Ser	Tyr	Arg	Gln	Gln	Arg	Val	Ser
65					70					75					80
Thr	Thr	Val	Thr	Gln	Asn	Asn	Asn	Ser	Glu	Phe	Ala	Trp	Pro	Gly	Ala
				85					90					95	
Ser	Ser	Trp	Ala	Leu	Asn	Gly	Arg	Asn	Ser	Leu	Met	Asn	Pro	Gly	Pro
			100					105					110		
Ala	Met	Ala	Ser	His	Lys	Glu	Gly	Glu	Asp	Arg	Phe	Phe	Pro	Leu	Ser
		115					120					125			
Gly	Ser	Leu	Ile	Phe	Gly	Lys	Gln	Gly	Thr	Gly	Arg	Asp	Asn	Val	Asp
	130					135					140				
Ala	Asp	Lys	Val	Met	Ile	Thr	Asn	Glu	Glu	Glu	Ile	Lys	Thr	Thr	Asn
145					150					155					160

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Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln Ser  
 165 170 175

Gly Gln Ala Gln Ala Ala Thr Gly Trp Val Gln Asn Gln Gly Ile Leu  
 180 185 190

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile  
 195 200 205

Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu  
 210 215 220

Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys  
 225 230 235 240

<210> SEQ ID NO 46  
 <211> LENGTH: 240  
 <212> TYPE: PRT  
 <213> ORGANISM: Adeno-associated virus-5

<400> SEQUENCE: 46

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser  
 1 5 10 15

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp  
 20 25 30

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln  
 35 40 45

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp  
 50 55 60

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly  
 65 70 75 80

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu  
 85 90 95

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr  
 100 105 110

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile  
 115 120 125

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu  
 130 135 140

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg  
 145 150 155 160

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser  
 165 170 175

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro  
 180 185 190

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp  
 195 200 205

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met  
 210 215 220

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn  
 225 230 235 240

<210> SEQ ID NO 47  
 <211> LENGTH: 9  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 47

Leu Ala Lys Asp Ala Thr Lys Asn Ala

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1 5

<210> SEQ ID NO 48  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 48

Pro Ala His Gln Asp Thr Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 49  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 49

Leu Ala His Gln Asp Thr Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 50  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 50

Leu Ala Thr Thr Ser Gln Asn Lys Pro Ala  
1 5 10

<210> SEQ ID NO 51  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 51

Leu Ala Ile Ser Asp Gln Thr Lys His Ala  
1 5 10

<210> SEQ ID NO 52  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 52

Ile Ala Arg Gly Val Ala Pro Ser Ser Ala  
1 5 10

<210> SEQ ID NO 53  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 53

Leu Ala Pro Asp Ser Thr Thr Arg Ser Ala  
1 5 10

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<210> SEQ ID NO 54  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 54

Leu Ala Lys Gly Thr Glu Leu Lys Pro Ala  
1 5 10

<210> SEQ ID NO 55  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 55

Leu Ala Ile Ile Asp Ala Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 56  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 56

Leu Ala Val Asp Gly Ala Gln Arg Ser Ala  
1 5 10

<210> SEQ ID NO 57  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 57

Pro Ala Pro Gln Asp Thr Thr Lys Lys Ala  
1 5 10

<210> SEQ ID NO 58  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 58

Leu Pro His Gln Asp Thr Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 59  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 59

Leu Ala Lys Asp Ala Thr Lys Thr Ile Ala  
1 5 10



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<210> SEQ ID NO 60  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 60

Leu Ala Lys Gln Gln Ser Ala Ser Thr Ala  
1 5 10

<210> SEQ ID NO 61  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 61

Leu Ala Lys Ser Asp Gln Ser Lys Pro Ala  
1 5 10

<210> SEQ ID NO 62  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 62

Leu Ser His Gln Asp Thr Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 63  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 63

Leu Ala Ala Asn Gln Pro Ser Lys Pro Ala  
1 5 10

<210> SEQ ID NO 64  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 64

Leu Ala Val Ser Asp Ser Thr Lys Ala Ala  
1 5 10

<210> SEQ ID NO 65  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 65

Leu Ala Ala Gln Gly Thr Ala Lys Pro Ala  
1 5 10

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<210> SEQ ID NO 66  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 66

Leu Ala Pro Asp Gln Thr Thr Arg Asn Ala  
1 5 10

<210> SEQ ID NO 67  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 67

Leu Ala Ala Ser Asp Ser Thr Lys Ala Ala  
1 5 10

<210> SEQ ID NO 68  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 68

Leu Ala Pro Gln Asp Thr Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 69  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 69

Leu Ala Lys Ala Asp Glu Thr Arg Pro Ala  
1 5 10

<210> SEQ ID NO 70  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 70

Leu Ala His Gln Asp Thr Ala Lys Asn Ala  
1 5 10

<210> SEQ ID NO 71  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 71

Leu Ala His Gln Asp Thr Lys Lys Asn Ala  
1 5 10

<210> SEQ ID NO 72

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<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 72

Leu Ala His Gln Asp Thr Thr Lys His Ala  
1 5 10

<210> SEQ ID NO 73  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 73

Leu Ala His Gln Asp Thr Thr Lys Lys Ala  
1 5 10

<210> SEQ ID NO 74  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 74

Leu Ala His Gln Asp Thr Thr Arg Asn Ala  
1 5 10

<210> SEQ ID NO 75  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 75

Leu Ala His Gln Asp Thr Thr Thr Asn Ala  
1 5 10

<210> SEQ ID NO 76  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 76

Leu Ala His Gln Gly Thr Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 77  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 77

Leu Ala His Gln Val Thr Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 78  
<211> LENGTH: 10

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<212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 78

Leu Ala Ile Ser Asp Gln Ser Lys Pro Ala  
 1                   5                   10

<210> SEQ ID NO 79  
 <211> LENGTH: 9  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 79

Leu Ala Lys Asp Ala Thr Lys Thr Ala  
 1                   5

<210> SEQ ID NO 80  
 <211> LENGTH: 9  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 80

Leu Ala Lys Asp Thr Thr Lys Asn Ala  
 1                   5

<210> SEQ ID NO 81  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 81

Leu Ala Lys Ser Asp Gln Ser Arg Pro Ala  
 1                   5                   10

<210> SEQ ID NO 82  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 82

Leu Ala Pro Gln Asp Thr Lys Lys Asn Ala  
 1                   5                   10

<210> SEQ ID NO 83  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 83

Leu Ala Thr Ser Asp Ser Thr Lys Ala Ala  
 1                   5                   10

<210> SEQ ID NO 84  
 <211> LENGTH: 10  
 <212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 84

Leu Ala Val Asp Gly Ser Gln Arg Ser Ala  
 1                   5                   10

<210> SEQ ID NO 85  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 85

Leu Pro Ile Ser Asp Gln Thr Lys His Ala  
 1                   5                   10

<210> SEQ ID NO 86  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 86

Leu Pro Lys Asp Ala Thr Lys Thr Ile Ala  
 1                   5                   10

<210> SEQ ID NO 87  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 87

Leu Pro Pro Gln Asp Thr Thr Lys Asn Ala  
 1                   5                   10

<210> SEQ ID NO 88  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 88

Pro Ala Pro Gln Asp Thr Thr Lys Asn Ala  
 1                   5                   10

<210> SEQ ID NO 89  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 89

Gln Ala His Gln Asp Thr Thr Lys Asn Ala  
 1                   5                   10

<210> SEQ ID NO 90  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 90

Leu Ala His Glu Thr Ser Pro Arg Pro Ala  
1                   5                   10

<210> SEQ ID NO 91  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 91

Leu Ala Lys Ser Thr Ser Thr Ala Pro Ala  
1                   5                   10

<210> SEQ ID NO 92  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 92

Leu Ala Asp Gln Asp Thr Thr Lys Asn Ala  
1                   5                   10

<210> SEQ ID NO 93  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 93

Leu Ala Glu Ser Asp Gln Ser Lys Pro Ala  
1                   5                   10

<210> SEQ ID NO 94  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 94

Leu Ala His Lys Asp Thr Thr Lys Asn Ala  
1                   5                   10

<210> SEQ ID NO 95  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 95

Leu Ala His Lys Thr Gln Gln Lys Met  
1                   5

<210> SEQ ID NO 96  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 96

Leu Ala His Gln Asp Thr Thr Glu Asn Ala  
1                   5                   10

<210> SEQ ID NO 97

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 97

Leu Ala His Gln Asp Thr Thr Ile Asn Ala  
1                   5                   10

<210> SEQ ID NO 98

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 98

Leu Ala His Gln Asp Thr Thr Lys Lys Thr  
1                   5                   10

<210> SEQ ID NO 99

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 99

Leu Ala His Gln Asp Thr Thr Lys Asn Asp  
1                   5                   10

<210> SEQ ID NO 100

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 100

Leu Ala His Gln Asp Thr Thr Lys Asn Thr  
1                   5                   10

<210> SEQ ID NO 101

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 101

Leu Ala His Gln Asp Thr Thr Lys Asn Val  
1                   5                   10

<210> SEQ ID NO 102

<211> LENGTH: 10

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic peptide

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&lt;400&gt; SEQUENCE: 102

Leu Ala His Gln Asp Thr Thr Lys Thr Met  
1 5 10

&lt;210&gt; SEQ ID NO 103

&lt;211&gt; LENGTH: 10

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic peptide

&lt;400&gt; SEQUENCE: 103

Leu Ala His Gln Asn Thr Thr Lys Asn Ala  
1 5 10

&lt;210&gt; SEQ ID NO 104

&lt;211&gt; LENGTH: 10

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic peptide

&lt;400&gt; SEQUENCE: 104

Leu Ala His Arg Asp Thr Thr Lys Asn Ala  
1 5 10

&lt;210&gt; SEQ ID NO 105

&lt;211&gt; LENGTH: 10

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic peptide

&lt;400&gt; SEQUENCE: 105

Leu Ala Ile Ser Asp Gln Thr Asn His Ala  
1 5 10

&lt;210&gt; SEQ ID NO 106

&lt;211&gt; LENGTH: 10

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic peptide

&lt;400&gt; SEQUENCE: 106

Leu Ala Lys Gln Lys Ser Ala Ser Thr Ala  
1 5 10

&lt;210&gt; SEQ ID NO 107

&lt;211&gt; LENGTH: 10

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic peptide

&lt;400&gt; SEQUENCE: 107

Leu Ala Lys Ser Asp Gln Cys Lys Pro Ala  
1 5 10

&lt;210&gt; SEQ ID NO 108

&lt;211&gt; LENGTH: 10

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic peptide



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<400> SEQUENCE: 108

Leu Ala Lys Ser Asp Gln Ser Lys Pro Asp  
1                   5                   10

<210> SEQ ID NO 109  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 109

Leu Ala Lys Ser Asp Gln Ser Asn Pro Ala  
1                   5                   10

<210> SEQ ID NO 110  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 110

Leu Ala Lys Ser Tyr Gln Ser Lys Pro Ala  
1                   5                   10

<210> SEQ ID NO 111  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 111

Leu Ala Asn Gln Asp Thr Thr Lys Asn Ala  
1                   5                   10

<210> SEQ ID NO 112  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 112

Leu Ala Pro Gln Asn Thr Thr Lys Asn Ala  
1                   5                   10

<210> SEQ ID NO 113  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 113

Leu Ala Pro Ser Ser Ile Gln Lys Pro Ala  
1                   5                   10

<210> SEQ ID NO 114  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 114

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Leu Ala Gln Gln Asp Thr Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 115  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 115

Leu Ala Tyr Gln Asp Thr Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 116  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 116

Leu Asp His Gln Asp Thr Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 117  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 117

Leu Asp His Gln Asp Thr Thr Lys Ser Ala  
1 5 10

<210> SEQ ID NO 118  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 118

Leu Gly His Gln Asp Thr Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 119  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 119

Leu Pro His Gln Asp Thr Thr Lys Asn Asp  
1 5 10

<210> SEQ ID NO 120  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 120

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Leu Pro His Gln Asp Thr Thr Lys Asn Thr  
1 5 10

<210> SEQ ID NO 121  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide  
  
<400> SEQUENCE: 121

Leu Pro His Gln Asp Thr Thr Asn Asn Ala  
1 5 10

<210> SEQ ID NO 122  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide  
  
<400> SEQUENCE: 122

Leu Thr His Gln Asp Thr Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 123  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide  
  
<400> SEQUENCE: 123

Leu Thr Lys Asp Ala Thr Lys Thr Ile Ala  
1 5 10

<210> SEQ ID NO 124  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide  
  
<400> SEQUENCE: 124

Leu Thr Pro Gln Asp Thr Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 125  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide  
  
<400> SEQUENCE: 125

Leu Val His Gln Asp Thr Thr Lys Asn Ala  
1 5 10

<210> SEQ ID NO 126  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide  
  
<400> SEQUENCE: 126

Leu Ala Lys Ala Asn Gln Asn Thr Pro Ala

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 1                    5                    10

<210> SEQ ID NO 127  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 127

Leu Ala Thr Thr Pro Ile Thr Lys Pro Ala  
 1                    5                    10

<210> SEQ ID NO 128  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 128

Leu Ala Thr Thr Pro Ile Ala Lys Pro Ala  
 1                    5                    10

<210> SEQ ID NO 129  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 129

Leu Ala Ile Glu Asp His Thr Lys Ser Ala  
 1                    5                    10

<210> SEQ ID NO 130  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 130

Leu Ala Gln Ser Glu His Gln Arg Pro Ala  
 1                    5                    10

<210> SEQ ID NO 131  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 131

Leu Ala Lys Ser Pro Asn Lys Asp Asn Ala  
 1                    5                    10

<210> SEQ ID NO 132  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 132

Leu Ala Asn Gln Asp Tyr Thr Lys Thr Ala  
 1                    5                    10

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<210> SEQ ID NO 133  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 133

Leu Ala Asn Ser Thr Asp Gln Thr Arg Ala  
 1                   5                   10

<210> SEQ ID NO 134  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 134

Leu Ala Leu Gly Glu Thr Thr Arg Pro Ala  
 1                   5                   10

<210> SEQ ID NO 135  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 135

Leu Ala Asn Ser Thr Glu Gln Thr Arg Ala  
 1                   5                   10

<210> SEQ ID NO 136  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 136

Leu Ala Gln Ala Asp Thr Thr Lys Asn Ala  
 1                   5                   10

<210> SEQ ID NO 137  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 137

Leu Ala Ser Lys Asp Ile Thr Lys Thr Ala  
 1                   5                   10

<210> SEQ ID NO 138  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 138

Leu Ala Ser Pro Arg His Asn Lys Lys Cys  
 1                   5                   10

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<210> SEQ ID NO 139  
 <211> LENGTH: 11  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 139

Leu Ala His Gln Asp Thr Thr Lys Thr Ile Ala  
 1                   5                   10

<210> SEQ ID NO 140  
 <211> LENGTH: 9  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 140

Leu Ala Ala Gln Gly Thr Ala Asn Leu  
 1                   5

<210> SEQ ID NO 141  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 141

Val Ala Ile Glu Asp His Thr Lys Ser Ala  
 1                   5                   10

<210> SEQ ID NO 142  
 <211> LENGTH: 12  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 142

Leu Ala Lys Ala Asn Gln Asn Thr Pro Lys Asn Ala  
 1                   5                   10

<210> SEQ ID NO 143  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (10)..(10)  
 <223> OTHER INFORMATION: Xaa is any amino acid

<400> SEQUENCE: 143

Leu Ala His Gln Asp Thr Thr Lys Lys Xaa  
 1                   5                   10

<210> SEQ ID NO 144  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide

<400> SEQUENCE: 144

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Leu Ala His Gln Asp Thr Thr Lys Lys Asp  
1 5 10

<210> SEQ ID NO 145  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide  
  
<400> SEQUENCE: 145

Leu Ala His Gln Asp Thr Thr Lys Lys Val  
1 5 10

<210> SEQ ID NO 146  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide  
  
<400> SEQUENCE: 146

Leu Ala His Gln Asp Thr Thr Lys Lys Met  
1 5 10

<210> SEQ ID NO 147  
<211> LENGTH: 7  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide  
  
<400> SEQUENCE: 147

Leu Gly Glu Thr Thr Arg Pro  
1 5

<210> SEQ ID NO 148  
<211> LENGTH: 11  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide  
<220> FEATURE:  
<221> NAME/KEY: Misc\_feature  
<222> LOCATION: (9)..(9)  
<223> OTHER INFORMATION: Xaa is Lys, Thr, Asn, or His  
<220> FEATURE:  
<221> NAME/KEY: Misc\_feature  
<222> LOCATION: (10)..(10)  
<223> OTHER INFORMATION: Xaa is Ala, Thr, Val, Ile, Met, or Asp  
<220> FEATURE:  
<221> NAME/KEY: Misc\_feature  
<222> LOCATION: (11)..(11)  
<223> OTHER INFORMATION: Xaa is Ala  
  
<400> SEQUENCE: 148

Leu Ala His Gln Asp Thr Thr Lys Xaa Xaa Xaa  
1 5 10

<210> SEQ ID NO 149  
<211> LENGTH: 10  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic peptide  
<220> FEATURE:  
<221> NAME/KEY: Misc\_feature  
<222> LOCATION: (3)..(3)  
<223> OTHER INFORMATION: Xaa is Ala, Pro, Asp, or His  
<220> FEATURE:

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<221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (5)..(5)  
 <223> OTHER INFORMATION: Xaa is Gly or Asp  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (7)..(7)  
 <223> OTHER INFORMATION: Xaa is Ala, Thr, or Lys  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (8)..(8)  
 <223> OTHER INFORMATION: Xaa is Asn, Glu, Lys, Arg, or Thr  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (9)..(9)  
 <223> OTHER INFORMATION: Xaa is Leu, Asn, Lys, or Thr  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (10)..(10)  
 <223> OTHER INFORMATION: Xaa is Ala, Thr, Asp, Val, or Met  
  
 <400> SEQUENCE: 149

Leu Ala Xaa Gln Xaa Thr Xaa Xaa Xaa Xaa  
 1                    5                    10

<210> SEQ ID NO 150  
 <211> LENGTH: 10  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (1)..(1)  
 <223> OTHER INFORMATION: Xaa is Val or Leu  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (3)..(3)  
 <223> OTHER INFORMATION: Xaa is Ile, Val, His, or Asp  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (4)..(4)  
 <223> OTHER INFORMATION: Xaa is Glu, Ser, Lys, or Gln  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (6)..(6)  
 <223> OTHER INFORMATION: Xaa is His, Ser, or Thr  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (9)..(9)  
 <223> OTHER INFORMATION: Xaa is Ser, Ala, Asn, His, or Lys  
  
 <400> SEQUENCE: 150

Xaa Ala Xaa Xaa Asp Xaa Thr Lys Xaa Ala  
 1                    5                    10

<210> SEQ ID NO 151  
 <211> LENGTH: 12  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic peptide  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (1)..(1)  
 <223> OTHER INFORMATION: Xaa is Leu  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (2)..(2)  
 <223> OTHER INFORMATION: Xaa is Ala  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (3)..(3)  
 <223> OTHER INFORMATION: Xaa is Lys, Leu, or Pro  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature



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<222> LOCATION: (5)..(5)  
 <223> OTHER INFORMATION: Xaa is Asn, His, Pro, or Tyr  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (7)..(7)  
 <223> OTHER INFORMATION: Xaa is Asn, Gly, Val, or Asp  
 <220> FEATURE:  
 <221> NAME/KEY: Misc\_feature  
 <222> LOCATION: (9)..(9)  
 <223> OTHER INFORMATION: Xaa is Pro or Thr

<400> SEQUENCE: 151

Xaa Xaa Xaa Ala Xaa Gln Xaa Thr Xaa Lys Asn Ala  
 1 5 10

<210> SEQ ID NO 152  
 <211> LENGTH: 27  
 <212> TYPE: RNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic sequence

<400> SEQUENCE: 152

cgcaaucagu gaaugcuuau acauccg

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What is claimed is:

1. A recombinant adeno-associated virus (rAAV) virion comprising:

- a) a variant AAV capsid protein, wherein the variant AAV capsid protein comprises an insertion of a heterologous peptide having a length of from 10 amino acids to 20 amino acids in the capsid protein GH loop relative to a corresponding parental AAV capsid protein, wherein the variant capsid protein confers increased infectivity of a retinal cell compared to the infectivity of the retinal cell by a control AAV virion comprising the corresponding parental AAV capsid protein, and wherein the heterologous peptide comprises the amino acid sequence LAKSDQSKPA (SEQ ID NO:61); and  
 b) a heterologous nucleic acid comprising a nucleotide sequence encoding a heterologous gene product.

2. The rAAV virion of claim 1, wherein the insertion site is between amino acids corresponding to amino acids 570 and 611 of VP1 of AAV2, or the corresponding position in the capsid protein of another AAV serotype.

3. The rAAV virion of claim 2, wherein the insertion site is located between amino acids corresponding to amino acids 587 and 588 of VP1 of AAV2, or the corresponding position in the capsid protein of another AAV serotype.

4. The rAAV virion of claim 1, wherein the gene product is:

- a) an interfering RNA or an aptamer;  
 b) a polypeptide; or  
 c) an RNA-guided endonuclease and a guide RNA.

5. The rAAV virion of claim 4, wherein the gene product is a polypeptide, and wherein the polypeptide is a neuro-protective polypeptide, an anti-angiogenic polypeptide, or a polypeptide that enhances function of a retinal cell, or an RNA-guided endonuclease.

6. The rAAV virion of claim 4, wherein the gene product is a polypeptide, and wherein the polypeptide is glial derived neurotrophic factor, fibroblast growth factor 2, neurturin, ciliary neurotrophic factor, nerve growth factor, brain derived neurotrophic factor, epidermal growth factor, rhodopsin, X-linked inhibitor of apoptosis, retinoschisin, RPE65, retinitis pigmentosa GTPase-interacting protein-1,

peripherin, peripherin-2, a rhodopsin, RdCVF, retinitis pigmentosa GTPase regulator (RPGR), Sonic hedgehog, or an RNA-guided endonuclease.

7. A pharmaceutical composition comprising:

- a) a recombinant adeno-associated virus virion of claim 1; and  
 b) a pharmaceutically acceptable excipient.

8. A method of delivering a gene product to a retinal cell in an individual, the method comprising administering to the individual a recombinant adeno-associated virus (rAAV) virion according to claim 1.

9. A method of treating an ocular disease, the method comprising administering to an individual in need thereof an effective amount of a recombinant adeno-associated virus (rAAV) virion according to claim 1.

10. An isolated nucleic acid comprising a nucleotide sequence that encodes a variant adeno-associated virus (AAV) capsid protein, wherein the variant AAV capsid protein comprises an insertion of a heterologous peptide having a length of from 10 amino acids to 20 amino acids in the capsid protein GH loop relative to a corresponding parental AAV capsid protein, and wherein the variant capsid protein, when present in an AAV virion, provides for increased infectivity of the AAV virion of a retinal cell, wherein the insertion is in the GH loop of a native AAV capsid, and

wherein the heterologous peptide comprises the amino acid sequence LAKSDQSKPA (SEQ ID NO:61).

11. The isolated nucleic acid of claim 10, wherein the insertion site is between amino acids corresponding to amino acids 570 and 611 of VP1 of AAV2, or the corresponding position in the capsid protein of another AAV serotype.

12. The isolated nucleic acid of claim 10, wherein the insertion site is between amino acids 587 and 588 of AAV2, between amino acids 590 and 591 of AAV1, between amino acids 575 and 576 of AAV5, between amino acids 590 and 591 of AAV6, between amino acids 589 and 590 of AAV7, between amino acids 590 and 591 of AAV8, between amino acids 588 and 589 of AAV9, or between amino acids 588 and 589 of AAV10.

**13.** A variant adeno-associated virus (AAV) capsid protein, wherein the variant AAV capsid protein comprises an insertion of a heterologous peptide having a length of from 10 amino acids to 20 amino acids wherein the insertion is in the GH loop of a native AAV capsid, and wherein the heterologous peptide comprises the amino acid sequence LAKSDQSKPA (SEQ ID NO:61). 5

**14.** The variant AAV capsid protein of claim **13**, wherein the insertion site is between amino acids corresponding to amino acids 570 and 611 of VP1 of AAV2, or the corresponding position in the capsid protein of another AAV serotype. 10

**15.** The variant AAV capsid protein of claim **13**, wherein the insertion site is between amino acids 587 and 588 of AAV2, between amino acids 590 and 591 of AAV1, between amino acids 575 and 576 of AAV5, between amino acids 590 and 591 of AAV6, between amino acids 589 and 590 of AAV7, between amino acids 590 and 591 of AAV8, between amino acids 588 and 589 of AAV9, or between amino acids 588 and 589 of AAV10. 15 20

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